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PAT 17-JAN-2001
CQ774324 Sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 6.2e-310;
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/note="unnamed protein product"
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1. 1377
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Patent: WO 0075319-A 15 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
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ARI37115 Sequence
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                                                                      September 23, 2005, 13:10:50 ; Search time 5974 Seconds (without alignments) 11168.870 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                      4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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Result Š.

	RESULT 2 AX056745 LOCUS LOCUS AX056745 LOCUS AX056745 LOCUS AX056745 LOCUS ACCESSION AX056745 VERSION AX0567	s,N.J., Davis,S. and Yancopon ineric polypeptides with imp 0075319-A 11 14-DEC-2000; HARMACEUTICALS, INC. (US) cation/Qualifiers 1453 rganism="Homo sapiens" ol_type="unassigned DNA" b xref="taxon:9606"	CDS 691445 (note="unnamed protein product"	SLSLSPGK" SLOWER SLOWER SLOWER SLOWER SLOWER SLOWER SLOWER Statement S
1 ATGGTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGTCTCTC 60	301 GGGCTTCTGACCTGTAAACAACTCAATGGGCATTTGTATAACACAAACTATCTCACA 360 301 GGGCTTCTCACCTGTGAAGCAACACTCAATGGGCATTTGTATAACACAAACTATCTCACA 360 301 GGGCTTCTCACCTGTGAACCAACACACACACTGTTGTATAACACAAACTATCTCACA 360 361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 420 421 TCTGTTGGAGAAAAGCTTGTTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT 480 421 TCTGTTGGAGAAAAGCTTGTTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGGATT 480	481 GACTTCAACTGGGAATACCCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540	601 GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660 661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACAGTGCCCACGTGC 720 661 AAGAACAGCACATTTGTCAGGGTCCATGAAAAGGACAAAACTCACACACA	841 GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGTGCATAATGCCAAGACA 900

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EVIVHENGPGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSH
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LSPGK"
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Homo sapiens
Eukaryota, metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidee; Homo.
                                                                      TATAGCAAGCTCACCCTGGGACAAGAGCAGGTGGCAGCAGGGGGAACGTCTTCTCATGCTCC
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llarity 86.7%; Pred. No. 1.4e-233;
Conservative 0; Mismatches 158; Indels 27;
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                                                                                                                                                                                                                                                                                  DNA
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Patent: WO 0075319-A 13 14-DEC-2000,
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 13 from Patent WO0075319.
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Matches 1201;
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             CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA
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/note="unnamed protein product"
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Properties
Patent: WO 0075319-A 5 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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/protein_id="CAC22374.1"
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PAT 17-JAN-2001

linear

DNA

AX056741 1389 bp Sequence 7 from Patent W00075319. AX056741

RESULT 5
AX056741
LOCUS
DEFINITION
ACCESSION

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Modified chimeric polypeptides with improved pharmacokinetic
properties
Patent: WO 0075319-A 7 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers 42; Length 1389; Indels 9 Score 1032.4; DB 6; Pred. No. 1.2e-229; 0; Mismatches 161; 1389 /note="unnamed protein product" /codon_start=1 1. 1389
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Best Local Similarity 85.5%;
Matches 1201; Conservative 61 ACAGGATCTAGTTCCGGA Homo sapiens Homo sapiens 412 181 셤 ð

Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D. Modified chimeric polypeptides with improved pharmacokinetic

Properties
Patent: WO 0075319-A 3 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers

1. .1674

'note="unnamed protein product"

codon start=1

/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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AUTHORS
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86.1%; Pred. No. 3.6e-219;
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17-JAN-2001

PAT

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DNA

Sequence 3 from Patent WO0075319.
AX056737.1 GI:12309716

RESULT 6
AX056737
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE

sapiens (human) sapiens

Homo Ношо

ORGANISM

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1

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Db 976 GAGCCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCCACCTGAACTCCTG 1035 Qy 739 GGGGACCGTCAGTCTTCCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 798 Db 1036 GGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG 1095 Qy 799 ACCCCTGAGGTCACATGCGTGGTGGACGACGACACCCTCAGGTCAAGTTC 858 Db 1096 ACCCTGAGGTCACATGCGTGGTGGACGACGACGACACACTCAAGTTC 1155 CQ 1096 ACCCTGAGGTCACATGCGTGGAGGTGCATAATGCCAAGACACACGAGGACACAGGTCAAGTTC 1155 CQ 1096 ACCCTGAGGTCACATGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGAGGAGGACAGGTCATAATGCCAAGACAAAAAGCCGCGGAGGAGGAGGAGGAGGAGGAG	Oy 919 TACAACAGCACGTACCGTGTGGTCACCGTCCTGCACCAGCACTGGCTGAT 978 DD	Oy 979 GGCAAGGGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC 1038	Oy 1039 ATCTCCAAAGCCAAAGCCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGG 1098	Oy 1099 GATGAGCTGACCAAGAACCAGGTCAGCTGACCTGGTCAAAGGCTTCTATCCCAGC 1158 DD 1396 GATGAGCTGACCAAGATCAGCTCAACCTGACCTGGTCAAAGGCTTCTATCCCAGC 1455	Oy 1159 GACATCGCCGTCGAGTCGGAGAGCAATGGGCAGCAGAGACAACTACAAGACCACGCCT 1218 Db 1456 GACATCGCCGTCGAGTCGCAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT 1515	Oy 1219 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAC 1278 Db 1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAC 1575	Oy 1279 AGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTATGAGGCTCTGCACACCAC 1338 Db 1576 AGGTGGAGAGGAAACGTCTTCTCATGCTCCTGTGATGCATGAGGTCTGGACAACCAC 1635	Oy 1339 TACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1377 Db 1636 TACACGCAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1674	AXO56743 AXO56743 LOCUS LOCUS LOCUS AXO56743 LOCUS ACCESSION AXO56743.1 G1:12309722 ACCESSION AXO6743.1 G1:12309722 KEYWORDS SOURCE Homo sapiens (human) ARAD6743.1 G1:12309722 REFERENCE Adminalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS AUTHORS AUGAILE AUTHORS Papadopoulos, N. J. Davis, S. and Yancopoulos, G. D. TITLE AUTHORS PERENCE AUGAILE AUTHORS AUGAILE AUGAI

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PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K"	Query Match 71.2%; Score 980.8; DB 6; Length 1704; Best Local Similarity 85.3%; Pred. No. 1.2e-217; Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;	Qy 79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTATACACATG 138	Qy 139 ACTGAAGGAAGCTCGTCATTCCCTGCGGGTTACGTCACCTAACATCACTGTTACT 198	Qy 199 TTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT 258 	Qy 259 AGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318	OY 319 GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATAGA 378	Qy 379 ATCATAGATGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGGTT 438	OY 439 GTCTTAAATTGTACAGCAAGAACTGAACTGAATGTGGGGGATTGACTTCAACTGGGAATAC 498	499 CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAAACCGAGACCTAAAAAACCCGGTCTGGG	DD 805 CCTGATGAAAAAATATAGAGAGGCTTCCGTAAGGCGACGAATTGACCAAAGCAAT 858 Qy 559 AGTGAGATGAAGAAATTTTTGAGCACCTTAACTATAGATGGTGTAACCGGAGTGACCAA 618	Db 859 TCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAAATGCAGAACAAAGAAA 918	Oy 619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAGAACAGCACATTTGTC 678	Qy 679 AGGGTCCATGAAAA	Qy 712 CCACCGTGCCCAGCACTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 771 Db 1039 CCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAA 1098	Qy 772 CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTG 831 Db 1099 CCCAAGGACACCCTCATGATCTCCCGGACCCTGAGGTCACATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	Oy 832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGACGGGGGGGG	1159 MCCACCAPAGACCCIGAGGICAACTICAACTGGAACGCGGGACGGGGTCAGGTCA	Db 1219 GCCAAGACACAGAGAGAGCAGTACAACAGCACGTACCGTGTGGTCACCTCTC 1278	QY 952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA 1011	17.79 ACCELCCTGCACCAGGACTGAATGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
Qy 892 GCCAAGACAAAAGCCGGGGAGGAGTACAACAGCACGTACCGTGTGGTCAGGTCCTC 951	Qy 952 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGGTACAAGGTCTCCAACAA 1011	OY 1012 GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGGCCAAAGGCCCCGAGAACCA 1071	Qy 1072 CAGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131	Qy 1132 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191 bb 1459 TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAATGGGCAG 1518	0y 1192 CCGGAGAACAACAACAACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC 1251	0y 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGGGAAGGGGGAACGTCTTCTCATGCTCC 1311	Qy 1312 GTGATGCATGAGGCTCTGCACAACAACAACAGAAGAGCCTCTCCCGGGT 1371	Oy 1372 AAATGA 1377 Db 1699 AAATGA 1704	RESULT 8	AXO56/35 LOCUS AXO56735 LOCUS AXO56735 DEFINITION Sequence 1 from Patent WO0075319. ACCESSION AXO56735		ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Elwaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Eutheria: Primates: Catarrhin: Hominidae: Homo.	Yancopoulos, G.D.	JOURNAL Patent: WO 0075319-A 1 14-DEC-2000; REGENERON PHARMACEUTICALS, INC. (US) FEATURES Location/Qualifiers	source 11704 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	CDS 11704 /note="unnamed protein product" /codon start=1 /roct=1 id="mac22372 1"	/ procenta=_x=z=z=z=z=z=z=z=z=z=z=z=z=z=z=z=z=z=z=	AGQTLALQCKGEARARWSLEERNOSKESEKLETTKSACCKNGKQFCSTITLENTAQANHI GFYSCKYLAVPTSKKGFTESATYIFISDTGRFPVENYSSEIPELIHPTEGRELVIPCRV TSPNITVTLKKFPLDTLIPQGKRITMDSRKGFIISNATYKEIGLLTCRATVNGHLYKT		GEFGSCURALITY FICTAL BELLOGGES YELF FERTAL LIMITSKIFE FYLCY Y DYGNEDFFE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA

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 1046 AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGC
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& Greve,J.M. and McClelland,A.
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Best Local Similarity 95.9
Matches 704; Conservative
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                  GCCCTCCCAGCCCCCATCGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA
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                                                             CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
                                                                                  CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
                                                                                                                            TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAAGCAATGGGCAG
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="fusion of human cDNA and Fc tag coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roczniak, S., Dubois-Stringfellow, N.A. and Zolotorev, A. Method of regulating anglogenesis using ryk protein. Patent: WO 0185789-A 17 15-NOV-2001;
Bayer Corporation (US)
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Sequence 17 from Patent W00185789.
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Best Local Similarity 99.6%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
     GCCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGGAGGAGCAGTACAACAGCACGTAC
                        GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGGAGTACAACAGCACGTAC
                                                                    CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
                                                                                    CGTGTGGTCGGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
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iive 0; Mismatches 0;
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/note="unnamed protein product"
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/organism="Homo sapiens"
/moltype="unassigned DNA"
/db xref="taxon:9606"
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Sequence 17 from Patent WO0238766.
AX556168
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/db_xref="GI:25899546"
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                                                 GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT
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Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 684; Conservative 0; Mismatches 0; Indels
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and response gene expression
Patent: US 6607879-A 1223 19-AUG-2003;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; E I (base 1 to 1019)

E Tao, W., Wong, S., Hickey, W.F., Hammang, J.P. and Baetge, E.E. Cell surface molecule-induced macrophage activation

L Patent: JP 2002528078-A 1 03-SEP-2002;
NEUROYDECH SA OS Homan)

PN JP 2002528078-A/1

PD 03-SEP-2002

PF 21-OCT-1999 JP 2000578449

PR 22-OCT-1999 US 09/178869

PI WENG TAO, SHOU WONG, WILLIAM F HICKEY, JOSEPH P HAMMANG, EDWARD E PI BAETGE
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JP 2002528078-A/1.
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                    GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
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1 (bases 1 to 1019)

1 Tao,W., Wong,S., Hickey,W.F., Hammang,J.P. and Baetge,E.Edward.
Cell surface molecule-induced macrophage activation
Patent: US 6197294-A 1 06-MAR-2001;
Location/Qualifiers
                                                                                                                                                                                             GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGGAGGAGGAGCAGTACAACAGCACGTAC
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100.0%; Pred. No. 1.7e-148;
cive 0; Mismatches 0;
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Seguence 1 from patent US 6197294.
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Search completed: September 23, 2005, 15:40:24 Job time : 5983 secs
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1 from patent US 6506891.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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RESULT 15 AR275187

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                                                                                                                                          Unclassified.

1 (bases 1 to 1019)

Tao, W., Wong, S., Hickey, W.F., Hammang, J.P. and Baetge, E.E.
Cell surface molecule-induced macrophage activation
Patent: US 656891-A 1 14-JAN-2003;
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September 23, 2005, 12:49:00; Search time 762 Seconds (without alignments) 10697.485 Million cell updates/sec Run on:

US-10-811-170-1 1377 Title: Perfect score:

1 atggtcagctactgggacac.......ccctgtctccgggtaaatga 1377 Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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N_Geneseq_16Dec04:* Database :

genesequ2000s:* genesequ2001as:* genesequ2001bs:* genesequ2002as:* geneseqn1980s:* geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:*

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SUMMARIES

1 1377 100.0 1377 5 AAA91076 2 1377 100.0 1377 6 ABQ74610 3 1328.4 96.5 1453 6 AAA91074 5 1049.2 76.2 1444 5 AAA91074 6 1049.2 76.2 1444 5 AAA91075 6 1049.2 76.2 1444 6 ABQ74609 1032.4 75.0 1389 6 AAA91071 10 1032.4 75.0 1389 6 AAA91072 11 987.4 71.7 1674 5 AAA91072 12 987.4 71.7 1674 5 AAA91070 13 982.4 71.3 1704 5 AAA91077 14 982.4 71.3 1704 5 AAA91077 15 980.8 71.2 1704 5 AAA91077 16 980.8 71.2 1704 6 ABQ74604 17 687.8 49.9 1299 10 AAL56123 18 687.8 49.9 1299 12 AAD010512	å Query Match Length DB ID	Description
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Aai67766 Human Ryk	Adc98597 Human ang	Adc98595 Human ang	Adc98593 Human ang	Adc98589 Human ang	Adc98591 Human ang	Adc98613 Human ang	Adc98587 Human ang	Adc98585 Human ang	Adc98567 Human ang	Aaq55340 tICAM(453	Aal56121 Plasmid p	Ado10508 Kb signal	Aaf57869 OPG-Fc co	Adi31897 Human cDN	Adl46173 Human imm	Abn89435 Human imm	Aad53735 Human wil	Aad53755 Human mod	Aad53760 Human mod	Adm68909 Human 1gG	Adl22760 Human ant	Adn97484 Artificia	Aaa53126 Human TR-	Aav34430 Antigenic
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ALIGNMENTS

Flt1 receptor fusion protein VEGFR1R2-FcDeltaC2 (a) coding sequence. Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region; ss. /product = "VEGFR1R2-FcDeltaC2(a)" Location/Qualifiers AAA91076 standard; DNA; 1377 BP. (first entry) ø 1. .137 /*tag= Unidentified 05-APR-2001 AAA91076; RESULT 1 Key

23-MAY-2000; 2000WO-US014142. WO200075319-A1 14-DEC-2000.

99US-0138133P.

18-JUN-1999;

Davis S, Yancopoulos GD; (REGE-) REGENERON PHARM INC. Papadopoulos NJ,

WPI; 2001-071076/08. P-PSDB; AAY97596.

Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model

Claim 9; Fig 24; 159pp; English.

This sequence encodes a fusion protein of the invention between the Flt1

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1020 1020 1080 1080 1140 1200 1200 1260

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Human, Flt1, vascular endothelial growth factor, VEGF, VEGF antagonist, psoriasis, wound healing, Flt1 receptor, antipsoriatic, antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic, ophthalmological, vascular permedblility, oedema, inflammation, asthma, brain oedema, inflammatory disorder, rheumatoid arthritis, burn, kidney disease, eye disorder, age-related macular degeneration,
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      AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCCTCACCGTCCTG
                       AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCACCGTCCTCACCGTCCTG
                                                               CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCCAACAAAGCCCTCCCA
                                                                                 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGAGTCCCCAACAACAAAGCCCTCCCA
                                                                                                                        GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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P-PSDB; ABP52449.
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receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve the harmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular
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to the mammal or human. A VEGF antagonist has antipsoriatic, antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, neptropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammatory associated with injury, oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes VEGFRIR2-
                                                                                                                                                                                                                                                                     enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic,
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CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTG
                                                                                                                                                                                                       832 AGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGAAATTATACACATGACTGAAGGAAGGGAGCTCGTCATTCCCTGCCGGGTTACGTCA 180
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                                                                                                                           Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
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                                     Yancopoulos GD
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Matches 1367; Conservative
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 REGENERON PHARM
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                                     Papadopoulos NJ,
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (WEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, cephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                               Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;
                                                                                 Location/Qualifiers
69. .1445
/*ttag= a //product= "Flt1D2.Flk1D3.FcDELTAC1(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Fig 21A-C; 179pp; English
                                                                                                                                                                                                                                                                                                                   Yancopoulos GD;
                                                                                                                                                                                                                      28-JAN-2002; 2002WO-US002466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                       fusion protein Flt1D2.VEGFR3D3.fcDeltaC1(a) DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAA
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                                                                                                                                                                                                                                                                                            receptor; fusion protein; chimeric protein; pharmacokinetic;
na leakage; vascular permeability; IgG Fc region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1049.2; DB 5;
Pred. No. 1.8e-244;
0; Mismatches 158;
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                                                                                BP
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86.7%;
                                                                                DNA; 1444
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                                                                                                                                                                                        entry)
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Matches 1201; Conservative
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                                                                                standard;
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                                                                                                                                                                                                                                          receptor
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antinflammatory, vulnerary, antiasthmatic, antinflammatory and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema associated with inflammatory disorders (e.g. rheumator) as the method as age-related asthma, burns, kidney diseases, or eye disorders such as age-related asthma, burns, kidney diseases, or eye disorders such as age-related used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present encodes
                                                                                                                                                                                                                                        psoriasis, wound healing, Fltl receptor, antipsoriatic, antiinflammatory, vulnerary, antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablility; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                      Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) nucleotide sequence
                                                                                                                                                                                                                        Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;
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69. .1436
/*tag= a
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                                                                                   standard; cDNA; 1444
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                                                                                                                                                    (first entry)
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Gaps

27;

Length 1444;

Score 1049.2; DB 6; Length Pred. No. 1.8e-244; 0; Mismatches 158; Indels

Query Match
Best Local Similarity 86.7%;
Matches 1201; Conservative

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                                                                                                           381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;
                                                                                  Indels
                                                      Score 1039; DB 5;
Pred. No. 5.3e-242;
0; Mismatches 170;
                                                     75.5%;
nilarity 86.3%;
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permeability in a mammal
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Matches 1189; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                             1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGGAGGGGGAACGTCTTCTCATGCTCC
                   CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
                                                      TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGAATGGGCAG
                                                                                  TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGAATGGGCAG
                                                                                                                                                                                                                                            GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
                                                                                                              CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTC
                                                                                                                                                                    TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGGGGGAACGTCTTCTCATGCTCC
                                                                                                                                                                                                                            GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein Mut2:Flt1(2-3deltaB)-Fc coding
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P-PSDB; AAY97591.
                                                                                                                                                                                                                                                                                                                                                                                      AAA91071 standard;
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CTCACCGTGGACAAGAGCAGGTGGCAGCAGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
                                                                                                                                                                                                                                               CTCACCGTGGACAAGAGCAGGTGGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Fll1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory; vulnerary; antisthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy; gene; ss.
                                                                                                                                                                                                                                                                       GAGGCTCTGCACACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTAAATGA 1377
                                                                                                                                                                                                                                                                                   Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF) antagonist.
                                               AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAATGGGCAGCCGGAGAAC
                                                                                                                                                                           AACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAG
                                   GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, rephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Mut2:Flil(2-3 delta B)-Fc which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;
Example 12; Fig 14A-C; 179pp; English.
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This sequence encodes a fusion protein of the invention between the Flti receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flti receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
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Pred. No. 2.2e-240;
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Yancopoulos
                                                                                                                                                                                                                                                                                   9; Fig 15; 159pp; English
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85.5%;
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Matches 1201; Conservative
Davis
                                                     WPI; 2001-071076/08.
P-PSDB; AAY97592.
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"Mut3:Flt1(2-3)-Fc protein"

/*tag= a /product= .1389

WO200260489-A1

Location/Qualifiers

Key

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                         GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
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Mutation 3 Flt1(2-3)-Fc nucleotide sequence ABQ74606 standard; cDNA; 1389 BP (first entry) 23-OCT-2002 ABQ74606;

Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;

sapiens Synthetic

diabetic retinopathy; gene; ss.

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chancing wound healing in a mammal or a human. The method comprises
administering a vascular endothelial cell growth factor (VBGF) antagonist
to the mammal or human. A VEGF antagonist has antipsoriatic,
antinflammatory, vulnerary, antiathmatic, antirheumatic, antiarthritic,
nephrotropic and ophthalmological activities. The method can be used in
treating psoriasis and enhancing wound healing in humans by administering
VBGF antagonist. The method is also useful in treating clinical
conditions characterised by vascular permeability, oedema or
inflammation, such as Brain oedema associated with injury, oedema
associated with inflammatory disorders (e.g. rheumatoid arthritis),
asthma, burns, kidney diseases, or eye disorders such as age-related
cmacular degeneration and diabetic retinopathy. The method may also be
used in making the polypeptide to decrease or inhibit plasma leakage and
or vascular permeability. The present sequence encodes Mut3:FILI(2-3)-FC
which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                  Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1032.4; DB 6; Length 1389; Pred. No. 2.2e-240; 0; Mismatches 161; Indels 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Fig 15A-C; 179pp; English
                                                                                                                                                                                                                               Yancopoulos GD;
                                                                                                               31-JAN-2001; 2001US-00773877
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Best Local Similarity 85.5%;
Matches 1201; Conservative
                                                                                                                                                                      (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                   WPI; 2002-608488/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 993
                                                                                                                                                                                                                                                                      526 CGAATTGACCAAAGCAATTCCCATGCCAACATATTCTACAGTGTTCTTACTATTGACAAA
CTTAGAGGCCATACTCTTGTTCTCTCAATTGTACTGCTACCACTCCCTTGAACACGAGGTT
                                                                                                                                           CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTGAGCACCTTAAACTATAGATGGT
                                                                                                                                                                                            GTAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG
                                                                                                                                                                                                                                                                                                                                                   TTCCTCTCCCCCCAAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
                                                                                                                                                                                                                                                                                                                                                                 TTCCTCTCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC
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                                       TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAAATGTGGGGATT
                                                                                                                  CAAATGACCTGGAGTTACCCT----GATGAAAAATAAGAGAGCTTCCGTAAGGCGA
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This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
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                                                                                                                                                                 Flt1 receptor fusion protein Mut1:Flt1(1-3deltaB)-Fc coding sequence.
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                                                                                                                                                                                                                    fusion protein, chimeric protein; pharmacokinetic; vascular permeability; IgG Fc region; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;
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Pred. No. 1.9e-229;
0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Flt1 (1-3deltaB) -Fc'
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AAA91070 standard; DNA; 1674
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Best Local Similarity 86.1%;
Matches 1119; Conservative
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plasma leakage;
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GCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACACATCGACAAACCAATACA
                                                                                                                                                                  ccigargaaárrgaccaaarrcccardccaacararrcracagrgrrcrracrarr
                                                                                                                                                                                                                        GACAAAATGCAGAACAAAGACAAAGGACTTTATACTTGTCGTGTAA---GGAGTGGACCA
                                                                                                                                                                                                                                                                                                           679 AGGGTCCATGAAAAGGACAAAACTCACACGTGCCCACCGTGCCCAGCACCTGAACTCCTG
                                                                                                                                                                                                                                                                                                                                                                  GGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
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                                                                                                                                      CCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAAACCGAGACCTAAAAAACCCAGTCTGGG
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                          ATCATAGATGTGGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAAGCTT
                                                                                  GTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATTGACTTCAACTGGGAATAC
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antiachmatic, antipheumatic, antiarthritic, antinflammatory, vulnerary, antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, vulnerary, antiachmatic, antinflammatory, by the method is also useful in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumator)d arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes Muti.FlL(1-3 delta B)-Fc which is used in an example from the present invention
                                                                                                                                                                                                                                                                                                                  psoriasis, wound healing; Flt1 receptor; antipsoriatic; antiinflämmatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 ACTGAAGGAAGGAGCTCGTCATTCCCTGCCGGGTTACGTCACCTAACATCACTGTTACT 198
                                                                                                                                                                                                                                                                                Human, Flt1; vascular endothelial growth factor, VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCCGAAATTATACACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Mut1:Flt1(1-3 delta B)-Fc protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                             Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 987.4; DB 6;
Pred. No. 1.9e-229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Fig 13A-D; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1674
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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ABQ74604 standard; cDNA; 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2001; 2001US-00773877.
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71.7%;
Best Local Similarity 86.1%;
Matches 1119; Conservative
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                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                      AB074604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
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1516 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCCCCGGAAATTATACACATG
                                                               385 AGIGATACAGGIAGACCITITCGIAGAGAIGIACAGIGAAAICCCCGAAATIAIACACAIG
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                                                                                                                                                                                                                                                                                                                                                                                            fusion protein; chimeric protein; pharmacokinetic; vascular permeability; 1gG Fc region; ss.
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                                                                                                                                                                                                                                                                                                                                                         receptor fusion protein Mut4:Flt1(1-3R-N)-Fc coding
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                                                                                                                                    1636 TACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1674
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Pred. No. 3.2e-228;
0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Flt1(1-3R-N)-Fc"
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                                                                                                                                                                                                                                                                                                                                                                                                fusion protein;
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71.3%;
Best Local Similarity 85.4%;
Matches 1132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davis S,
                                                                                                                                                                                                                                                                                                                       (first entry)
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P-PSDB; AAY97593.
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                                                                                                                                                                                                                                                                                                                                                                                                                 plasma leakage;
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AAA91073
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                                                                                                                                  AGAAAGGCCTTCATCATATCAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA
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TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT
                                                                                    TTAAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT
                                                                                                                                                                                                                                                                                  ATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTATCTGTTGGAGAAAGCTT
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VBGF) antagonist to the mammal or human. A VBGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VBGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammatory as an inceptated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related
                                                                                                                                                                                                                                                                                                       Mutation 4 Flt1(2-3 R->N)-Fc nucleotide sequence.
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                                                                                                          CAGGTGTACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC
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                                                                                                                                                                                                                                                                                  TTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAACGCATAATCTGGGACAGT
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macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 >N)-Fc which is used in an example from the present invention
                                                                                                                                     Gaps
                                                                                                                                   33;
                                                                                                     Score 982.4; DB 6; Length 1704; Pred. No. 3.2e-228; 0; Mismatches 161; Indels 33;
                                                                          Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;
                                                                                                       Query Match
71.3%;
Best Local Similarity 85.4%;
Matches 1132; Conservative
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This sequence encodes a fusion protein of the invention between the Flt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
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Pred. No. 7.8e-228;
0; Mismatches 162; Indels 33;
                                                                                                                                                                                   Sequence 1704 BP; 508 A; 460 C; 386 G; 350 T; 0 U; 0 Other;
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Best Local Similarity 85.3%;
Matches 1131; Conservative
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ò	1012	GCCTCCCAGCCCCATGAGAAACCATCTCCAAAGCCAAAGGCAGCCCCGAGAACCA 1071
ΟD	1339	GCCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA 1398
λΌ	1072	CAGGIGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1131
οp	1399	CAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACC 1458
ò	1132	TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
ΟD	1459	TGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGAAAAGGCCAG 1518
δλ	1192	CCGGAGAACAACTACAAGACCACGCCTCCCGTGGACTCCGACGGCTCCTTCTTCCTC 1251
Dþ	1519	CCGGAGAAACAACTACAAGAACCACCCCCCCCGTGCTGCTCCTCCTCCTTCCT
λŏ	1252	TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGAGAACGTCTTCTCATGCTCC 1311
ΩÞ	1579	TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCC 1638
ò	1312	GTGATGCATGAGGCTCTGCACACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1371
qq	1639	GIGATGCATGAGGCTCTGCACAAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT 1698
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US-10-811-170-1 1377 Title: Perfect score:

1 atggtcagctactgggacac.......scctgtctccgggtaaatga 1377 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

68479088 34239544 segs, 19032134700 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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9b est1: 9b est2: 9b htc: 9b est4: 9b est6: 9b 9s81: 9b 9s82: EST:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

BG753979 871 bp mRNA linear EST 15-MAY-2001 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence. BG753979 1 GI:14064632 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Buraryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo	1 (bases 1 to 871) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCML686 row: k column: 02	High quality sequence stop: 848. Location/Qualifiers 1871 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="laxon:9606" /clone="IMAGE:4846201" //clone="IMAGE:4846201" //clone="IMAGE:4846201" //clone="IMAGE:4846201" //clone="INAGE:486201" //clone="Type="primary B-cells from tonsils (cell line)" //lab host="DRINB (phage=resistant)" //clone="Type="primary B-cells", Vector: porms; Site_1: XhoI; //clone="Typ	
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMR469 row: k column: 12
High quality sequence stop: 604.
Location/Qualifiers
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(Dases 1 to 983)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
49.7%; Score 684; DB 4; Le
100.0%; Pred. No. 4.7e-179;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xrefe"taxon:9606"
/db_xrefe"taxon:9606"
/db_nost="Daylous"
/clone="twasp:5:4609"
/clon
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603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
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1 (bases 1 to 843)

11 HMGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab host="DH10B (phage-resistant)"
/clone=lib="NIH MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site 1: Xhol; Site 2: BCoRI; cDNA made by oligo-dT priming. Directionally cloned into BcoRI/Xhol sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                          AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Endit: Gapts Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Properation: Robert Matson
Cond Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                          GACAAAACTCACACTGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCTCAGTC
                                                                                                                                                                   TTCCTCTTCCCCCCAAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
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                                                                                                                                                  TTCCTCTTCCCCCCAAAACCCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                              Gaps
                                                           ö
                             Length 843;
                                                           Indels
                            Score 682.4; DB 4;
Pred. No. 1.3e-178;
0; Mismatches 1;
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5', mRNA Sequence.
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                                                           683; Conservative
                                          Best Local Similarity
Matches 683; Conser
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AUTHORS
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cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM216 row: m column: 22
High quality sequence stop: 739.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoP V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                         1294 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1353
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full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
                                                                                                                                                        743 AACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
                                                                                                                                                                                                                                                 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC
                                                                                                                                                                                                                                                                                                                                863 GACGGCTCCTTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGAGGGGGG
                                           GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG
                                                                                                                                                                                                                     TGGGAGAGCAATGGGCAGCCGGAGACAACTACAAGACCACGCCTCCCGTGCTGGACTCC
                                                                                      683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG
                                                                                                                                 1114 AACCAGGTCAGCCTGACCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="csoD10404Na16"
/tissue_type="Placenta_Cot_25-normalized"
/plasmid="pcWVSPORT_6"
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llarity 99.9%; Pred. No. 1.4e-178;
Conservative 0; Mismatches 1;
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CRS95172.1 GI:50475979
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Homo sapiens (human)
Homo sapiens
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Matches 683; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 ERNY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                            CR611254 1022 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens
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648 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAGAAGAGC 707
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/plasmid="pCMVSPORT_6"
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/db_xref="taxon:9606"
/clone="CS0DE007VJ17"
                                                           CTCTCCCTGTCTCCGGGTAAATGA 731
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HTC; CNSLT_CDNA.
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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers

1. 1090

/organism="Hono sapiens"
/mol_type="mRNA"
/db xref="Laxon:9606"
/clone="CSODIO71YG21"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pcMVSPORT_6"
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Pred. No. 1.4e-178;
0; Mismatches 1;
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Catarrhini, Hominidae, Homo.
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Placenta Cot
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Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases 1 to 1090)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                     1294 AACGICTICICAIGCICCGIGAIGCAIGAAGGCICIGCACAACCACTACACGCAGAAGAGC 1353
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                                 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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full-length cDNA clone CS0D1048YC07 of Placenta Cot 25-normalized
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO48YCO7"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
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CR616804.1 GI:50497611
HTC; CNSLT_CDNA.
HOMO sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. Li (bases 1 to 1091)
Li W. B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
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/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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CR604961.1 GI:50485768
HTC; CNSLT_CDNA.
Homo sapiens (human)
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HTC; CNSLT_CDNA.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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  Score 682.4; DB 3;
Pred. No. 1.4e-178;
0; Mismatches 1;
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVAY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoN V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases 1 to 1098)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
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full-length cDNA clone CS0CAP001YII3 of Thymus of Homo sapiens
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/organism="Homo sapiens"
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/clone="CSOCAPOOIYII3"
/tissue_type="Thymus"
/plasmid="pCMVSPORT_6"
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HOMO SADIENS (human)
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Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Catarrhini; Hominidae; Homo.
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full-length cDNA clone CSOCAP008YF07 of Thymus of Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia, Butheria, Primates, Catarrhini, Hon
11 (bases 1 to 1102)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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99.9%; Pred. No. 1.4e-178;
iive 0; Mismatches 1;
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/clone="CSOCAP008YF07"
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/plasmid="pcMVSPORT_6"
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Homo sapiens (human)
Homo sapiens
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Direct Submission

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr

Web : www.genoscope.cns.fr)

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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RO1081YF02"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Direct Submission
Submitted (20-UUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

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Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, cDNA libraries and normalization
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TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC
                                                                             GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGGAGCAGTACAACAGCACGTAC
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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full-length cDNA clone CS0DI059YL06 of Placenta Cot 25-normalized
of Homo sapiens (human).
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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                  AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1;
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/clone="CSODE010YH13"
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/plasmid="pcMvSPORT_6"
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// cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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sequence 11, Appl Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 1120, Ap Sequence 52, Appli Sequence 52, Appli Sequence 22, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 23, Appli Sequence 24, Appli Sequence 25, Appli Sequence 26, Appli Sequence 27, Appli		DRY SKIN DISEASES	Length 1377; Indels 0; Gaps 0;	TGCTCAGCTGTCTGCTTCTC 60	TAGAGATGTACAGTGAAATC 120	ATTCCCTGCCGGGTTACGTCA 180	CTTTGATCCCTGATGGAAAA 240 	aatgcaacgtacaagaaata 300 atgcaacgtacaaagaaata 300	ATAAGACAACTATCTCACA 360
4 US-09-383-916-11 3 US-08-487-550-7 4 US-09-526-098-7 4 US-08-030-175-6 4 US-08-030-175-6 4 US-08-030-175-7 4 US-08-030-175-7 4 US-09-499-846-5 4 US-09-499-846-5 4 US-09-746-3594-52 4 US-09-746-3594-52 4 US-09-313-942-23 1 US-08-476-25-2 2 US-08-476-25-2 4 US-09-313-942-23 1 US-08-476-275-2	ALIGNMENTS	S/09773877B t al. DS FOR TREATING INFLAMMATORY R: US/09/773,877B 1-01-31 n 3.0 n 3.0 lence 1R2.FcdeltaC1(a) Receptor	100.0%; Score 1377; DB 4; 100.0%; Pred: No. 0; ive 0; Mismatches 0;	ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCT 	ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATCT 	CCGAAATTATACACATGACTGAAGGAAGCTCGTCATTCCCTGCCGGTTACGTCA 	ctaacatcactgttactttaaaaagtttccacttgacactttgatccctgatggaaaa 	GGCATAATCTGGGACAGTAGAAAGGGCTTCATCATCAAATGCAACGTACAAAGAAATA 	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA
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		RESULT 1 US-09-773-877B-25 Sequence 25, Appl FREENL NO. 683334 GENERAL INFORMATI TITLE OF INVENT: FILE REFERENCE: CURRENT APPLICAT CURRENT PILING DI NUMBER OF SEQ ID SOFTWARE: PAECH SEQ ID NO 25 LENGTH: 1377 TYPE: DNA CRGANISM: ARLIÉ FEATURE: CRANISM: ARLIÉ FEATURE: COGANISM: ARLIÉ FEATURE: COCATION: (1) US-09-773-877B-25	Query Match Best Local S Matches 1377	Qy Dp	Oy 6	Qy 12 Db 12	Oy 18	Qy 241 Db 241	Qy 30 Db 30
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        APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 110b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 1453
                                                                                                                                                                                                                                                      Length 1453;
                                                                                                                                                                   FEATURE:
COTHER INFORMATION: F1t1D2.F1k1D3.FcdeltaC1(a)Receptor
NAME/KEY: CDS
LOCATION: (69)..(1442)
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96.5%; Score 1328.4;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches
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SENERAL INFORMATION:
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Sequence 21, Application US/09773877B Patent No. 6833349 RESULT 2 US-09-773-877B-21

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ORGANISM: Artificial Sequence
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US-09-773-877B-17
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Sequence 15, Application US/09773877B
Sequence 15, Application US/09773877B
Sequence 15, Application US/09773877B
SEQUENCE NO. 1978A-100:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REPERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT PILING DATE: 2001-01-31
NUMBER OF SEQ 1D NOS: 27
SEQ 1D NOS: 27
SEQ 1D NO 15
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Pred. No. 3.5e-268;
0; Mismatches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Flt1(2-3 deltaB)-Fc(Mut2)
NAME/KEY: CDS
LOCATION: (1)..(1359)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.5%;
86.3%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 1189; Conserv
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US-09-773-877B-15
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                                              766 TTCCTCTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1114 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
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                                                                                                                                          CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOSTWARE: Patentin version 3.0
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86.1%; Pred. No. 2.6e-254;
iive 0; Mismatches 171;
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Best Local Similarity 86.1
Matches 1119; Conservative
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US-09-773-877B-13
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US-09-773-877B-13
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            APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                                                                                       Length 1389
                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.0%; Score 1032.4; DB 4; Length Best Local Similarity 85.5%; Pred. No. 2.1e-266; Matches 1201; Conservative 0; Mismatches 161; Indels
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                                                                                                                                                                                                                                                                   (Mut 3)
                                                                                                                                                                                                                                                               OTHER INFORMATION: Flt1(2-3)-Fc
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(1389)
US-09-773-8778-17
GENERAL INFORMATION
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                                          CCCGTGCTGGACTCCGACGCCTCCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGC
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                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: XIA, YU-PING et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT APPLICATION NUMBER: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                         71.3%; Score 982.4; DB 4;
85.4%; Pred. No. 5.7e-253;
live 0; Mismatches 161;
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                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/09773877B Patent No. 6833349
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Matches 1132; Conserv
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US-09-773-877B-19
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                                                                                                                                                                                                                                                                             Score 980.8; DB 4;
Pred. No. 1.5e-252;
0; Mismatches 162;
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                                                                                                                                      OTHER INFORMATION: Flt1(1-3)-Fc NAME/KEY: CDS
                             LENGTH: 1704
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 85.3
Matches 1131; Conservative
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US-09-773-877B-11
SEQ ID NO 11
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                NAME/KEY: tICAM(453)/IgG fusion
OTHER INFORMATION: bp 1-1359 = nucleotides coding
OTHER INFORMATION: for amino acid residues 1-453 of ICAM-1; bp 1360-
OTHER INFORMATION: 2040 = nucleotides coding for amino acid residues
OTHER INFORMATION: 216-442 of human heavy chain IgG1; bp 2401-2043 =
OTHER INFORMATION: stop codon
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                                                                                                                                             MOLECULE TYPE: other nucleic HYPOTHETICAL: no
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95.9%;
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TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2043 Dp
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.9
Matches 704; Conservative
                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                              linear
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FEATURE:
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                 ACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
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                                                                                                  GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCCAAAGGGCAGCCCCGAGAACCA
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US-08-27-496C-14
Sequence 14, Application US/08227496C
Sequence 14, Application US/08227496C
Patent No. 6130202
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
TITLE OF INVENTION: Multimeric Forms of Human
TITLE OF INVENTION: Multimeric Forms of Human
MUMBER OF SEQUENCES: 20
CORRESPONDENCES: 20
CORRESPONDENCES: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 1.44 Mb storage
COMPUTER: Dell Optiles GXI
CORRATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 8.0 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,496C
FILING DATE: 04/14/94
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APPLICATION NUMBER: 07/903,069
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/704,984
FILING DATE: 05/24/91
APPLICATION NUMBER: 07/556,238
FILING DATE: 07/20/90
ATTORNEY, AGENT INFORMATION:
NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MT 214.2C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                             425 AACCAGGTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 484
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245 CGTGTCGTCACCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 304
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APPLICANT: Wong, Shou
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REPERENCE: 17810-043
CURRENT FILING DATE: 1988-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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NAME/KRY: gene
LOCATION: (). )
OTHER INFORMATION: Polynucleotide
OTHER INFORMATION: Polynucleotide
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49.7%; Score 684; UB 3; Lo
Best Local Similarity 100.0%; Pred. No. 4e-173;
Matches 684; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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; LOCATION: (16)..(1008)
US-09-178-869-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 684; DB 4; Lo
Pred. No. 3.4e-173;
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49.7%; Score 684; DB
Best Local Similarity 100.0%; Pred. No. 3.4
Matches 684; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                3: INCYTE PHARMACEUTICALS, INC
3174 PORTER DRIVE
                                                                                                          Sequence 1223, Application US/09023655; Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESSI:
ADDRESSEE: INCTTE PHARMACEUTICALS, STREET: 3174 FORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Zeller, Karen J.
REGISTATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1223:
SEQUENCE CHARACTERISTICS:
2030 CTCCGGGTAAATGA 2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CLONE: 9243865
US-09-023-655-1223
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                                                                                                US-09-023-655-1223
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684; Conservative
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US-09-180-100-18
Query Match
Best Local Similarity
Matches 684; Conserv
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                       748 AACCAGGTCAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
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APPLICANT: Tao, Weng
APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hommang, Shou
APPLICANT: Hommang, Joseph P.
APPLICANT: Hammang, Joseph P.
APPLICANT: Bactege, E. Edward
TILLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT FILING DATE: 2001-01-16
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: gene
LOCATION: ()...)

OTHER INFORMATION: Description of Sequence: Recombinant:
OTHER INFORMATION: Polynucleotide
NAME/KEY: CDS
LOCATION: (16)..(1008)
US-09-761-413-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTCCCTGTCTCCGGGTAAATGA 1377
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Patent No. 6506891
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ORGANISM: Homo sapiens
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US-09-761-413-1
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APPLICANT: NAKAMURA, No. 6306395io
TITLE OF INVENTION: NOVEL FAS ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER APPLICATION NUMBER: PCT/JP97/01502
SAFLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 1182
49.7%; Score 684; DB 4; L
100.0%; Pred. No. 4e-173;
iive 0; Mismatches 0;
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985 CGTGTGGTCACCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGAGAGTACAAG 1044
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                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: TECKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET UNBER: 35,030
TELECOMMULCATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-621
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
49.7%; Score 684; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0;
                                                                                                            COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear _ MOLECULE TYPE: DNA (genomic)
                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1428 base pairs
                     United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                               COMPUTER READABLE FORM:
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                       COUNTRY: United
ZIP: 22313-1404
Virginia
                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-08-488-376-19
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Betent No. 5811524

GENERAL INFORMATION:

APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: PAN, Li-Zhen
APPLICANT: WALSH, Edward E.
APPLICANT: WERRD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
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                       Length 1182;
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                49.7%; Score 684; DB 3; Le
100.0%; Pred. No. 4.2e-173;
ive 0; Mismatches 0;
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                                                               684; Conservative
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ADDRESSEE: Burns, Do
STREET: P.O. Box 140
CITY: Alexandria
                                        Similarity
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US-08-488-376-19
; Sequence 19, Ap
                Query Match
Best Local S
Matches 684
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Search completed: S
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APPLICANT: BRAMS, Peter
APPLICANT: CHANAT, Soulaima Salim
APPLICANT: HANAT, Soulaima Salim
APPLICANT: HERANT, Cheryl Janne
APPLICANT: HERED, Cheryl Janne
APPLICANT: HERED, Cheryl Janne
APPLICANT: HERED, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HICH AFFINITY HUMAN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
1285 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGG 1344
                            GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCCGTCAGTC 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BR PC Compatible
COMPUTER: PatentIN Release #1.0, Version #1.30
SOCTWARE: PatentIN Release #1.0, Version #1.30
SOCTWARE: PatentIN Release #1.0, Version #1.30
FILING DATE: PATENTION DATA:
PRIOR APPLICATION NUMBER: US/08/634,223
FILING DATE: O7-UN-1995
ATTORNEY/AGBRY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 49.7%; Score 684; DB 2; Lo
Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                         3: Burns, Doane, Swecker & Mathis
P.O. Box 1404
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6201
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                       CTCTCCCTGTCTCCGGGTAAATGA 1377
                                                                                                       ; Sequence 19, Application US/08634223
; Patent No. 5840298
; GENERAL TWICE
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LOCATION:
US-08-634-223-19
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APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: VEGFRIR2.FcdeltaCl(a) Receptor NAME/KEY: CDS
1. LOCATION: (1)..(1377)
VS-09-773-877A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1377;
.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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; Sequence 25, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
PEATURE:
 Query Match
Best Local Similarity
Matches 1377; Conserv
SEQ ID NO 25
LENGTH: 1377
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Sequence 1, P
Sequence 1, P
Sequence 1, P
Sequence 9, P
Sequence 9, P
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Sequence 9,
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                                                                                                   September 23, 2005, 13:48:22 ; Search time 932 Seconds
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(cgn2 6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
(cgn2 6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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(cgn2 6/ptodata/2/pubpna/USO0_PUBCOMB.
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               5.1.6
Compugen Ltd.
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US-10-609-775-9
US-10-860-958-1
US-10-830-902-1
US-10-897-802-1
US-10-890-021-9
US-10-909-011-3
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                version = 2005 (
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                GenCore (c) 1993
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Maximum DB seq length: 200000000
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Sequence

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US-10-998-243-15
US-11-016-097-15
US-10-998-881-3
US-10-999-144-1
US-10-999-11-1
US-10-998-243-11
US-10-998-243-11
US-10-998-243-11
US-10-998-243-13
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Publication No. US20040014667A1;
GENERAL INFORMATION:
APPLICANT: Thomes D. Fand;
APPLICANT: Nicholas J. Papadopoulos
ITILE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
FILE REFERENCE: REG 710D
CURRENT APPLICATION NUMBER: US/10609,775
CURRENT APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-33
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTERED for Windows Version 4.0
SEQ ID NOS: 25
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           APPLICANT: Huang, Jianzhong
APPLICANT: Yancopoulos, George
APPLICANT: Rudge, John
TITLE OF INVENTION: Method of Tumor Regression with VEGF
TITLE OF INVENTION: Inhibitors
FILE REPERENCE: REG 714A
CURRENT APPLICATION NUMBER: US/10/860,958
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 60/476,425
PRIOR APPLICATION NUMBER: 60/476,425
PRIOR PLING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FRAEESEQ for Windows Version 4.0
SEQ ID NO 1
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ive 0; Mismatches
Yamashiro, Darrell
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Best Local Similarity 100.
Matches 1377; Conservative
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US-10-860-958-1
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Sequence 1, Application US/10860958 Publication No. US20040265309A1 GENERAL INFORMATION: APPLICANT: Kandel, Jessica APPLICANT: Holash, Jocelyn

RESULT 3 US-10-860-958-1

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   CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC
                                  GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
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Sequence 1, Application US/10830902

Sequence 1, Application US/10830902

Publication No. USZO050004027A1

GENERAL INFORMATION:

APPLICANT: Stanley Wiegand

APPLICANT: Claus Cursiefien

TITLE OF INVENTION: Method of Treating Corneal Transplant

TITLE REFERENCE: REG 713B

CURRENT APPLICATION NUMBER: US/10/830,902

CURRENT FILING DATE: 2004-04-23

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: homo sapiens
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APPLICANT: Jocelyn Holash
APPLICANT: Jocelyn Holash
APPLICANT: Jocelyn Holash
APPLICANT: George Yancopoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REPRENCE: REG 716A
CURRENT APPLICATION NUMBER: US/10/909,011
CURRENT FILING DATE: 2004-07-30
PRIOR FILING DATE: 2003-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3-1
                                                                                                   CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1020
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ive 0; Mismatches
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; Publication No. US20050112061A1
; GENERAL INFORMATION:
; APPLICANT. ---
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Matches 1377; Conservative
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CURRENT FILING DATE: 2004-06-29
FRIOR APPLICATION NUMBER: 10/609,775
FRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 29
SECTIANGE FREUSEQ for Windows Version 4.00
LENGTH: 1377
TYPE: DNA
CRANISM: homo sapiens
US-10-880-021-9
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JAPPLICANT: Wiegand, Stanley
APPLICANT: Papadopoulos, Nicholas J.
APPLICANT: Papadopoulos, Gordon
APPLICANT: Papadopoulos, Gordon
APPLICANT: Papadopoulos, Gordon
TITLE ON INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Pro
TITLE OF INVENTION: and Methods of Making and Using Thereof
FILE OF INVENTION: and Methods of Making and Using Thereof
FILE OF INVENTION: and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/988,243
CURRENT APPLICATION NUMBER: 10/009,852
PRIOR FILING DATE: 2004-11-12
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: DNA
                   CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320
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                                  1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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; Publication No. US20050175610A1
; GENERAL INFORMATION:
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US-10-988-243-15
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Best Local Similarity
Matches 1377; Conserv
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US-10-988-243-15
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100.0%; Score 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/998,881
CURRENT FILING DATE: 2004-11-29
FRIOR APPLICATION NUMBER: 10/909,011
PRIOR PILING DATE: 2004-07-30
FRIOR PILING DATE: 2000-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5: SEQ ID NO 5: 4
LENGTH: 1377
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; ORGANISM: homo sapiens
US-10-998-881-3
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Publication No. US20050196340A1
GENERAL INFORMATION:
APPLICANT: JocelyH Holash
APPLICANT: George Yanocpoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REFERENCE: 716B
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Publication No. US20050163798A1
GENERAL INFORMATION:
APPLICANT: Nicholas J. Papadopoulos et al.
TITLE OF INVENTION: PHARMACKINETIC POLYPEPTIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT APPLICATION NUMBER: US/11/016,097
CURRENT PILING DATE: 2004-12-17
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 38
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LENGTH: 1377
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100.0%; Score 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismarches
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
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100.0%; Pred. No. 0;
live 0; Mismatches
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Fublication No. US20050197291A1
GENERAL INFORMATION:
APPLICANT: Stanley Wiegand
APPLICANT: Glaus Cursiefied
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
APPLICANT: Glaus Cursiefied
TITLE OF INVENTION: Rejection In High Risk F
FILE REFERENCE: 713C
CURRENT APPLICATION NUMBER: US/11/039,144
CURRENT FILING DATE: 2005-01-19
FRIOR FILING DATE: 2004-04-23
FRIOR FILING DATE: 2004-04-23
FRIOR FILING DATE: 2000-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity 100.
Matches 1377; Conservative
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ORGANISM: homo sapiens
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Publication No. US20040014667A1
GENERAL INFORMATION:
APPLICANT: Thomas J. Daly
APPLICANT: James P. Fandl
APPLICANT: Nicholas J. Papadopoulos
TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEI
CURRENT APPLICATION NUMBER: US/10/609,775
CURRENT FILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: 10/009,852
PRIOR APPLICATION NUMBER: PCT/US00/14142
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/138,133
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FRAESEO for Windows Version 4.0
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Matches 1367; Conservative
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                        Length 1453;
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                                                                                                                                                                                     OTHER INFORMATION: Flt1D2.Flk1D3.FcdeltaC1(a)Receptor
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                                                                                                                                                                                                                                                                    96.5%; Score 1328.4;
98.6%; Pred. No. 0;
live 0; Mismatches
                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (69)..(1442)
US-09-773-877A-21
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Best Local Similarity
Matches 1367; Conserval
                                                                                                                     LENGTH: 1453
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APPLICANT: Jocelyn Holash
APPLICANT: George Yancopoulos
APPLICANT: George Yancopoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REPERBNCE: REG 716A
CURRENT APPLICATION NUMBER: US/10/909,011
CURRENT APPLICATION NUMBER: 60/492,864
PRIOR FILING DATE: 2003-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                        Sequence 1, Application US/10909011;
Publication No. US20050112061a1
GENERAL INFORMATION:
APPLICANT: George Yancopoulos
APPLICANT: Phyllis R. Wachsberger
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.6%;
Matches 1367; Conservative 0
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US-10-909-011-1
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                                          CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATTGAACTA 479
                                                                                                        TCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGGATT 539
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 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419
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Search completed: September 23, 2005, 17:12:40 Job time : 937 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Q8n4y9 h	O6mzx7 L	Q68cn4 h	Q8nf17 h	P01860 h	P01870 c	Q95m34 e	P01862 c	Q7tmk1 m	P22436 m	P03987 m	Q6pip8 n	Q65zq1 }	0991c4 n
Q8N4Y9	Q6MZX7	Q68CN4	QBNF17	GC3 HUMAN	GC RABIT	Q95M34	GC2 CAVPO	Q7TMK1	GC3 MOUSE	GC3M MOUSE	QGPIP8	065201	Q99LC4
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46.9	46.6	46.6	46.4	. 46.2	38.0	37.6	36.9	35.8	35.6	35.1	35.0	34.9	34.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 VGEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL-----QSSGLYSLSSVVTV 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
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A Qi Y., Xiang J.;
A Qi Y., Xiang J.;
I. A genetically engineered single-gene-encoded anti-TAG72 chimeric artibody secreted from myeloma cells.";
I. Hum. Antibodies Hybridomas 6:161-166(1995).
R EMBL; 882493; AABS7424.:;
R INTERPO: IPR003599; Ig. C.
R INTERPO: IPR003506; Ig. MHC.
R Pfam: PF07654; Cl-set; Z.
R Pfam; PF00654; Cl-set; Z.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                           85;
                                                                                                 Query Match 52.0%; Score 1267.5; DB 2; Length 466; Best Local Similarity 55.8%; Pred. No. 8.3e-80; Matches 281; Conservative 34; Mismatches 104; Indels 85;
PROSITE; PS00290; IG MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50853 MM; 53EB0BCEDE81076E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLV------NRD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGL-MTKKNSTFVRVHEK----DKTH
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.4%; Score 1253.5; DB 2; Length 487; Best Local Similarity 64.5%; Pred. No. 8.2e-79; Matches 260; Conservative 29; Mismatches 67; Indels 47;
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SWART; SM00409; IG; 3.
SWART; SM00409; IGc1; 2.
SWART; SM00406; IGc2; 2.
SWART; SM00406; IGv; 2.
PROSITE; PSS0835; IG LIKE; 4.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein DKFZp686P15220.
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Best Local Similarity 62.4%
Matches 262; Conservative
                                                sequences.
                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
    S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6MZQ6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O6MZQ6
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1D Q6
00 D7
00 D7
00 D7
00 D8
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X TISSUE-Primary B-Cells;

X Stausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Stausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altansner R.D. Collins P.S., Wanner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.P., Jordan H., Moore T., Wans J.T., Wang J., Habteh F.,

A Hopkins R.P., Jordan H., Moore T., Wax S.I., Wang J., Habteh F.,

B Archardes C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

W Williang M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                          G-FIIS-----NATYKEIGLLTCEATV------NGHLYKTNYLTHRQTNTIIDV- 130
                                                                                                                                                                                                                                                                                                       131 -----VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRD 180
                                                                                                                                                                                                                                                                                                                                                                                                   ----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNH----KPSNTKVDKRVEPKSCDKTHT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPPCPAPELLGGGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 430
                                                                                                                                                                                     88
                                                                                                                                                                                                                              34 GRSLRLSCAASG-----FTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIAYADSVK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LKTQSGSEMKKFLSTLT1DGVTRSDQGLYTCAASSGLMTKKNSTFV--RVHEK--DKTHT
                                                                                                                                         Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                     75;
                                                                                           DB 2; Length 472;
                                                                                       Query Match 51.4%; Score 1252.5; DB 2; Length Best Local Similarity 59.1%; Pred. No. 9.3e-79; Matches 273; Conservative 24; Mismatches 90; Indels
                                                                                                                                                                                   GRELVIPCRVTSPNITVTLKKFPLDTLI-----PDGKRIIW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                             26CB340D0046D279 CRC64;
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Last annotation update)
PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                        ll protein.
472 AA; 51724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypochetical protein. Homo gapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                   Hypothetical
SEQUENCE 47
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GKRIIW------DSRKG-FIIS-----NATYKEIGLLTCEATV-----NGH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 LYKTNYLTHRQTNTIIDV------VLSPSHGIELSVGEKLVLNCTARTELNVGID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
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           full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VSWNSGALTSGVHTPPAVL-----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 HEDPEVKFNWYVDGVEVHNAXTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQQNVFSCSVWHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 FNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 TKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                         Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018747; AAH18747.1; -.
HSSP; P01861; IADQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ll protein.
470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;
"Generation and initial analysis of more than 15,000 and mouse cDNA sequences.";
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein DKFZp686G11190.
Name=DKFZp686G11190;
                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.4%; Score 1252; DB 2
62.4%; Pred. No. 1e-78;
tive 23; Mismatches 6
                                                                                                                                                                                                                                                                                 InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR0003597; IG.21;
InterPro; IPR003597; IG.21.
InterPro; IPR003596; IG.21.
InterPro; IPR003596; IG.21.
InterPro; IPR004596; IG.22.
SMART; SM00407; IG.22.
SMART; SM00407; IG.21; 3.
SWART; SM00407; IG.21; 3.
PROSITE; PS50835; IG.LIKE; 4.
PROSITE; PS508290; IG.MIC; UNKNOWN_2.
Hypothetical protein.
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AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Score 1246; DB 2;
61.6%; Pred. No. 2.7e-78;
ive 23; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835, IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-C1.
InterPro; IPR003596; IG MHC.
InterPro; IPR003596; IG MHC.
InterPro; IPR004596; IG MHC.
InterPro; IPR004596; IG MHC.
INTERPRO; IPR00459; IG SWART; SW00409; IG; 2
SWART; SW00407; IGC1; 3.
                                                                                                                                                                                                                                                                                                            BC041037; AAH41037.1;
P01861; 1ADQ.
                                                                                                                                                                                                                             cDNA sequences.
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es 265; Conservative
                                                                                                                                                                                                                                                                             IISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein
SEQUENCE 478 AA;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Proc. Natl. Acad.
                                                                                                                                                                                                                             and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                EMBL;
HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVIHQDWLNGKEYKCKVS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472
                                                                                                                                                                                                                                                                                                                                                LTHRQT-----NTIIDVVLSPSHGIEL-----SVGEKLVLNCTARTELNV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQKSLSLS
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                                                                                                                                                                                                                                                                                                                      GKGLEWVSGISSSGVNTYYADSVKGRFTISGDISTNTLYLQMHSLRADDTAVYYCARADY
                                                                                                                                                                                                                                                                                                                                                                      RDYQVSPAYWYFDVWGRGTLVSVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
                                                                                                                                                                                                                                                                                                                                                                                               GIDFNWE---YPSSKHOHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                              GLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                             Gaps
                          Fobo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                            51;
                          Α.,
                                                                                                                                                                                                                                                    Length 475;
       The German Human CDNA Consortium;

A Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A Han M., Walemann S.;

A Han M., Walemann S.;

B Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX640947; CAE45972.1; -.

R HSSP; P01861; JADO.

InterPro; IPR001359; Ig.:

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001359; Ig.:

R InterPro; IPR001359; Ig.:

R InterPro; IPR001359; Ig.:

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 1.

R PROSITE; PS00290; IG IGV; 1.

R PROSITE; PS00290; IG IG INKE; 4.
                        C., Osanger
                                                                                                                                                                                                                                                                            88; Indels
                                                                                                                                                                                                                l protein.
475 Aa; 52043 MW; B7EAE255A26F4B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                               51.1%; Score 1240...;
61.0%; Pred. No. 2.4e-78;
five 26; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           478
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  TISSUE=Human esophagus tumor;
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27,
27,
                                                                                                                                                                                                                                                               Best Local Similarity 61.0
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel. Hypothetical protein. Homo sapiens (Human).
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TISSUE=Primary B-Cells;
                                                                                                                                                                                                                                                                                                   GKRIIW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGK 475
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                                                                                                                                                                                                                   Hypothetical
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                                                                                                                                                                                                                                                                                                                          61
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Straubberg R.L., Feingold E.A., Grouse L.H., Dorge J.G., Klausner R.D., Collins F.S., Wagner L.H., Dorge J.G., Straubberg R.L., Feingold E.A., Grouse L.H., Dorge J.G., Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Chenztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | | : | | | | | | | | GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQWNSLRAEDTAVYYCAREFE
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Altachur R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul R.E., Zeeberg B., Buerow K.H., Schaefer C.F., Bhata N.K.,

Hopkins R.F., More T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Hilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krywinski M.I., Sakaiska U., Smailus D.E., Schnerch A., Schein J.E.,

Jand mouse CDNA sequences."

Jand mouse CDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------NTIIDV-----VLSPSHGIELSVGEKLVLNCTARTELNVGIDFNW 164
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                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
IISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, BC073766; AMH73766.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig. c1.
InterPro; IPR003597; Ig c1.
InterPro; IPR003506; Ig w.
Pfam; PF00647; Ig. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                    465 AA
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
                                                                                                                                                 PRT;
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(TrEMBLrel. 27, L
(TrEMBLrel. 27, L
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SMART; SM00407; IGc1; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                               PRELIMINARY;
                                       469 OKSLSLSPGK 478
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Homo sapiens (Human)
449 QKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altachul R. Collins F.S., Wagner L.H., Derge J.G.,

Altachul S.F., Zeeberg B., Buerow K.H., Schmenn C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buerow K.H., Schmefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hoste F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brans S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Sarchenko S., Sanchez A.,

Whiting M., Madan A., Young A.C., Bevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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119 FTYFDYWGQGTLVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFPEPVTVSW 176
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                                                                                                                                                                     177 NSGALTSGVHTFPAVL-----QSSGLYSLSSVVTVPSSSLGTQ-TYICNVNHKPSNTK
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                                                                                    E---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKK
                                                                                                                                                                                                                                                     222 NSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Strausberg R.;
Strausberg R.;
Submitted (UTW-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO13/713, AAH73773.1; -.
InterPro; IPR001599; Ig.
InterPro; IPR001599; Ig.
InterPro; IPR001506; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR003106; Ig.
InterPro; IPR001596; Ig.
InterPro; IPR0047; ig.; 4.
SMART; SM00409; IG; 2.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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482
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InterPro; IPR003597; 1g - 1.

InterPro; IPR003596; 1g - W.

Pfam; PF07064; C1-set; 3.

Pfam; PF00047; ig; 4.

SMART; SM00409; IG; 2.

SMART; SM00406; IGC; 1.

PROSITE; PS00290; IG_IKE; 4.
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                                                                  and mouse cDNA sequences.
Proc. Natl. Acad. Sci. U.
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                                                                                                         SEQUENCE FROM N.A.
TISSUE=Spleen;
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                                                                                                                                                                61 PPGKGLEW---IGYIYYSGSTYYNPSLKSRVTISLDTSRNQFSLKMNSVTAADTAVYFCA
                                                                                                                                                                                                   -----VLSPSHGIBLSVGEKLVLNCTA
                                                                                                                                                                                                                                                                                                          TCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
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Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                77 PDGKRIIWDSRKGFI-ISNATYKEIGL----LTCEATVNGHLYKTNYLTHRQT----
                                                                                                                       Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                      90;
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TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                              Length 476;
                                                                                                                       Indels
                                                                    CRC64;
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Last annotation update)
                                                                                            51.1%; Score 1245; DB 2; 60.8%; Pred. No. 3.1e-78; ive 23; Mismatches 85;
                                                    Hypothetical protein.
SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  475
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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                                                                                                                      261; Conservative
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Hypothetical protein.
Homo sapiens (Human).
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85 DSRKG-FIIS----NATYKEIGLLTCE-----ATVNG----HLYKTNYLTHRQTN 125
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 DSVKGRFTISRDNYKNTLYLQLGSLRAEDKAVYYCARARCRGDTCLNFYYGLDVWGQGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 TIIDVV------YPSSKHQIELSVGEKLVLNCTARTELNVGIDFNWE---YPSSKHQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073782; AH737982.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
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475 AA; 51987 MW; 2AIFE55D736860F8 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp686N02209.
                                                                                                                                                                          Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 51.1%; Score 1244.5; DB 2; Best Local Similarity 64.4%; Pred. No. 3.4e-78; Matches 261; Conservative 19; Mismatches 84;
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"The nucleotide sequence of a human imm
Nucleic Acids Res. 10:4071-4079(1982).
  Berson B.J., Hood L.E.;
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MEDLINE=81208100; PubMed=7236608;
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PubMed=826475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intrachain disulfide bonds.
                                                                                                                                                                                                                                                                                    (MYELOMA
                                                                                                                                                                                                                                                                                   SEQUENCE (MYELOMA MEDLINE=77070269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                   34 GRSLRLSCIASGFSFSGSAMHWLROIP-----GKGLEWVAVISYDGNHKLYSDSVKGR
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                                      TISSUB=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Subo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX38118; CAD98026.1; --
HSSP; P01857; 11ZH.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                             73;
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                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                              51.0%; Score 1242.5; DB 2; Length
57.1%; Pred. No. 4.7e-78;
ive 27; Mismatches 100; Indels
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                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;
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(Rel. 45, Last annotation update)
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PROSITE; PS00290; IG MHC; UNKNOWN_2.
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MEDLINE=82274238; PubMed=6287432;
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21-JUL-1986 (Rel. 01, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                     Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003065; Ig_MHC.
Interpro; IPR0035965; Ig_V.
Pfam; PF07654; CI-8et; Ig_V.
                                                                                                                                                                                                                                                                                                          Matches 266; Conservative
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Name=1GHG1;
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SMART; SM00406; IGv; 1.
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NCBI_TaxID=9606;
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DE 19 9a

GN Homo

OC Bukar

OC Mamma

OC NCBI

RN [1]

RR RN [1]

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its Ponstingl H., Hilschmann N.,
"The rule of antibody structure. The primary structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
peptides of the H-chain, alignment of the tryptic peptides and
discussion of the complete structure.",
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976). the Amino Amino immunoglobulin C gammal gene."; MEDLINE-83289131; PubMed-6884994; Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."; Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983). MEDIINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Schwarz J., Reichel W., Hilschmann N.;
Schwarz St., Reichel W., Hilschmann G., and monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromde cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976). -!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and G1M(11) markers, 239-D and 241-L. KOL and EU sequences have the G1M(1) markers and the G1M (non-1) markers and the G1M (non-1) markers in the amidation states of 35, 116, 198, 269 and 272.
-!- MISCELLANEOUS: EU also differs in the amidation states of resit 155, 166, 177, 195, 198, 269, and 272 and in the order of resit 268-272. human gamma G-immunoglobulin. VII. A cyanogen bromide fragments H1-H4."; "The covalent structure of a human gamma G-immunoglobulin. 8. Am: acid sequence of heavy-chain cyanogen bromide fragments H5-H7."; Biochemistry 9:3171-3181(1970). "Crystallographic refinement and atomic models of a human Fc fragand its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution.";
Biochemistry 20:2361-2370(1981). of SEQUENCE OF 136-329 (EU). MEDLINE=71064025; PubMed=5530842; Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H., MEDLINE=71064027; PubMed=4923144; Gall W.E., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. X. -!- MISCELLANEOUS: KOL also differs in the amidation states MEDLINE=71064024; PubMed=5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M., "The covalent structure of a human gamma G-immunoglobulin. acid sequence of heavy-chain cyanogen bromide fragments H1-Biochemistry 9:3161-3170(1970). SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS. SEQUENCE OF 1-135 (MYELOMA PROTEIN EU) ANGSTROMS).

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PRELIMINARY;
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330 AA;
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   IGHG1 protein.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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K -> R (in GlM(3) marker).

FT-GEVAR 00388.

D-> E (in GlM(non-1) marker).

FTIGEVAR 003887.

L -> M (in GlM(non-1) marker).

FTIGEVAR 003888.
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Interchain (with heavy chain)
Interchain (with heavy chain)
                                                            EMBL; J00228; AAC82527.1; ALT_INIT.

PIR; A93433; GHHU.

R PDB; 1AJ7; X-ray; H=1-101.

PDB; 1D51; X-ray; H=1-101.

R PDB; 1D51; X-ray; H=1-101.

R PDB; 1D51; X-ray; H=1-101.

R PDB; 1D6V; X-ray; H=1-101.

R PDB; 1D6V; X-ray; A/B=106-329.

R PDB; 1EK; X-ray; A/B=106-329.

R PDB; 1FCC; X-ray; A/B=106-329.

R PDB; 1FCC; X-ray; A/B=106-329.

R PDB; 1IX; X-ray; A/B=107-330.

R PROSUTE; PSC00290; 1G_MHC; 2.

R PROSUTE; PSC00290; 1G_MHC; 1.

R PROSUTE; PSC00290; 1G_MHC; 2.

R PROSUTE; PSC00290; 1G
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                                                                                                                                                                                                                             231 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                        197 TIDGVTRSDQGLYTCAA----SSGLMT-----KKNSTFV--RVHEK--DKTHTCP
                                                                                                                                                                  52 TFPAVLQS-SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP
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                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                          19;
                                         Query Match 50.9%; Score 1240.5; DB 1; Length 330; Best Local Similarity 86.4%; Pred. No. 4e-78; Matches 242; Conservative 7; Mismatches 12; Indels 19;
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TISSUE=Spleen;
MEDILNE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
36106 MW; 3770EE106C2FA33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq)
01-ORT-2004 (TrEMBLrel. 26, Last ann
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A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brange C., A Brapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., A Willalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Jones S.J., Marra M.A.;
R. "Generation and initial analysis of more than 15,000 full-length human D.M. A Marios Chun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%; Score 1240.5; DB 2; Length
86.4%; Pred. No. 6.3e-78;
ive 7; Mismatches 12; Indels
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC051328; AAH51328.1; -.
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003506; Ig_rMc.
InterPro; IPR003566; Ig_v.
Pfam; PF07654; C1-set; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS000350; IG_LIKE; 4.
PROSITE; PS000290; IG_MC; UNKNOWN 2.
SEQUENCE 469 AA; 51395 MW; C8D58B12BAAF795C CRC64;
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                                                                                                                                                                                                                                and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 86.4 les 242; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                           HSSP; P01857; 1HZH.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                        rissum=Spleen;
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schamen C.M., Schuler G.D.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcinci P., Prange C.,
A Richards S., Worley K.C., Hale S., Garcinci P. Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 TIDGVTRSDQGLYTCAA----SSGLMT-----KKNSTFV--RVHEK--DKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.9%; Score 1240.5; DB 2; Length 470; 86.4%; Pred. No. 6.3e-78;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Strauberg R.;
Submitted (MD-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC053984; AAH53984.1; --
HSSP; P01887; IHZH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfan; PP07654; C1-eet; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.4
Matches 242; Conservative
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Search completed: Sombleted: Some 124 secs
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 GKRIIW------DSRKG-FIIS-----NATYKEIGLLTCEATVNGHLYKTNY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VVLSPSHGIELSVGEKLVLNCTARTELNV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 GLMTKKNSTFV--RVHEK--DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 ----KPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPFKPKDTLMISRTPEVT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLITVLHQDWLNGKEYK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 WESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 HTSPWYPSFFDYWGQGILVTVSSASTKGPSVFPLAPSS--KSTSGGTAALGCLVKDYFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 GIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (ANG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX640853; CAE45920.1; -- HSSP; P01861; 1ADQ.
                                                                                               Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52121 MW; 9476EAE4COBFC447 CRC64;
       annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.9%; Score 1239.5; DB Best Local Similarity 61.6%; Pred. No. 7.5e-78; Matches 263; Conservative 25; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348 AA
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003597; IG.
InterPro; IPR003597; IG.
InterPro; IPR003596; IG.
InterPro; IPR03596; IG.
InterPro; IPR03596; IG.
INTERPROSITE; IPR0369; IG.
INTERPROSITE; INTERPROSITE; INTERPROSITE; IG.
INTERPROSITE; INTERPROSITE INTERPROSITE; INTERPROSITE; INTERPROSITE INTERPROSI
05-JUL-2004 (TrEMBLrel. 27, Last and
Hypothetical protein DKFZp686C11235
Name=DKFZp686C11235;
                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Human small intestine;
The German Human cDNA Consortium;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein
SEQUENCE 473 AA;
                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSLSPGK 458
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                                                                                                                                            NCBI_TaxID=9606;
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Q6PYX1
ID Q6PYX:
AC Q6PYX:
DT 05-JUI
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Created) Last sequence update)

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358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 KTKPREEQYNSTYRVUSULTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 PCPAPELLGGBSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 TIDGVTRSDQGLYTCAA----SSGLMT-----KKNSTFV--RVHEK--DKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 VYTLPPSRDELTKNOVSLICLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLY
                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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                                                                                                                                                                                                                                                    Zhu N.S., Chen Y.Y.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; ARS70731; AAS88328.1; -.
HSSP; P01857; Jad7.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR00710; Ig-like.
InterPro; IPR0031006; Ig-MC.
InterPro; IPR003597; Ig-Cl.
InterPro; IPR003587; Ig-Cl.
SMART; SMART; SMO0407; IGL1; 3.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS508396; IG-MHC; UNKNOWN_2.
                              B virus receptor binding protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                    Homo sapiens (Human)
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                                                                                                                                                                 NCBI_TaxID=9606;
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                Copyright
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- protein search, using sw model protein September 23, 2005, 14:00:46 ; Search time 120 Seconds (without alignments) 1476.135 Million cell updates/sec Run on:

US-10-811-170-2

2437

1 MVSYMDTGVLLCALLSCLLL.....MHEALHNHYTQKSLSLSPGK score: Title: Perfect :

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: genesecol9Anc.* Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay97596 Flt1 rece	Abp52449 Modified	Aay97594 Flt1 rece		Abp52450 Flt1D2.Fl	Aay97595 Flt1 rece		Aay97592 Flt1 rece	Abp52445 Mutation			Aay97593 Flt1 rece	Abp52446 Mutation			Aay97590 Flt1 rece	Abp52443 Mutation	_	_	MVP-A	9 MVP-A	Aar48037 tICAM(453	Abu07273 Human exp	Abw02188 Human IL-	Adp76035 AMIGO pol
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Score	2437	2437	2399	2399	2275.5	2069.5	2069.5	2049	2049	2038	2038		2015.5	2014.5	2014.5	2003.5	2003.5	1726.5	1716	1627.5	1619.5	1304	1304	1293.5	1292
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ALIGNMENTS

Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region. Flt1 receptor fusion protein VEGFRIR2-FcDeltaC1(a). Ā AAY97596 standard; protein; 458 (first entry) 05-APR-2001 AAY97596; RESULT 1

WO200075319-A1.

14-DEC-2000

23-MAY-2000; 2000WO-US014142.

99US-0138133P. 08-JUN-1999;

(REGE-) REGENERON PHARM INC

Yancopoulos GD;

Davis S,

Papadopoulos NJ,

WPI; 2001-071076/08. N-PSDB; AAA91076.

Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model systems.

Claim 49; Fig 24; 159pp; English.

This sequence represents a fusion protein of the invention between the Fl1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal

Sequence 458 AA;

Query Match

100.0%; Score 2437; DB 4; Length 458;

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The piresult invention and amount or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist control and amamal or human. A VEGF antagonist has antipostriatic, antianthrial cantinflammatory, vulnerary, antiathmatic, antirheumatic, antianthrial cantinflammatory, vulnerary, antiathmatic, antirheumatic, antianthrial conspiration in promises and enhancing wound healing in humans by administering to VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or conditions characterised by vascular permeability, oedema or conditions that inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumator) associated with inflammatory disorders (e.g. rheumator) as age-related castuma, burns, kidney diseases, or eye disorders such as age-related consecutation and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents invention
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               administration of a vascular endothelial cell growth factor (VEGF)
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100.0%; Pred. No. 1.1e-153;
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                                                                                                   invention describes a method
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ABP52447 standard; protein; 458 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVYTLPPSRDELTKNQVSLICLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
                                                                                                                                                                                                                                                                                                                                                       This sequence represents a fusion protein of the invention between the Fl1 receptor and the Fc region of 19G. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                 Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPCPAPELLGGPSVFLFPPKRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%; Score 2399; DB 4; Length 458; 98.7%; Pred. No. 3.9e-151; ive 0; Mismatches 0; Indels
                                                                                                                                                                             Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                             Claim 49; Fig 21; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular permeability in a mammal
                                                                                     23-MAY-2000; 2000WO-US014142.
                                                                                                                  99US-0138133P
                                                                                                                                               (REGE-) REGENERON PHARM INC
                                                                                                                                                                             Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455; Conservative
                                                                                                                                                                                                       2001-071076/08.
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                                                                                                                                                                             Papadopoulos NJ,
                                                                                                                                                                                                                       N-PSDB; AAA91074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 458 AA;
                          WO200075319-A1
Unidentified.
                                                                                                                  08-JUN-1999;
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The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, empirotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related uscular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents
                                                                                                                                                         psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablility; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
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                                                             Modified Flt1 receptor Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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Pred. No. 3.9e-151;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Fig 21A-C; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2002; 2002WO-US002466.
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REGE-) REGENERON PHARM INC
(first entry)
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                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200260489-A1
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23-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458

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administrating a vacular manner of the method can be used in treating psoriasis and enhancing wound healing in humans by administering very manner. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain cedema associated with inflammatory discases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents

Pitid2 Fikid3 FCDELTACI(a) which is used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNH 420
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comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2275.5; DB 5;
Pred. No. 5.8e-143;
0; Mismatches 0;
wound healing in a mammal or a human.
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Best Local Similarity
Matches 429; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 432 AA;
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AAY97595
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                         HRQINIIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 177
                                                                                                                       LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKGPGDKTHTC 237
                                                                                                                                                                                                       PPCPAPELLGGPSVFLFPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
                                                                                                                                                                                                                                                                                              AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
                                                                                      LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                           QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                                                                                                                                                                    AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                             PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flt1D2.Flk1D3.FcDELTAC1(a) protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy.
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Disulfide-bond
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||||||| : : | | | | HINDINITIDIOLIPRESIBLE SERVETAN SEVIFOND YPGKQAERGKWVPER 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354
                                                                                                                                                                                                                                       This sequence represents a fusion protein of the invention between the Flt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 57
                                                                                                                                                       Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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                                                                                                                                                                                                                                                                                                                                                                  84.9%; Score 2069.5; DB
85.7%; Pred. No. 3e-129;
ive 16; Mismatches 4.
                                                                                                g
                                                                                                 Yancopoulos
                                                                                                                                                                                                                                                                                                                    vascular permeability in a mammal
                                                                                                                                                                                                                    Claim 49; Fig 22; 159pp; English.
                         2000WO-US014142
                                                99US-0138133P.
                                                                      (REGE-) REGENERON PHARM INC
                                                                                              Davis S,
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                      WPI; 2001-071076/08,
                                                                                                                                                                                                                                                                                                                                                                              al Similarity
395; Conserv
                                                                                              Papadopoulos NJ,
                                                                                                                                   N-PSDB; AAA91075
                                                                                                                                                                                                                                                                                                                                            Sequence 455 AA;
                        23-MAY-2000;
                                                08-JUN-1999;
 14-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
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chiancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antiposoriatic, antianthermatic, as bean conditions characterised by vascular permeability, oedema or associated with injury, oedema or associated with injury, oedema associated with injury, oedema or associated with injury, oedema or usersociated with injury, oedema or usersociated with injury, oedema or macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                          psoriasis, wound healing; Flti receptor; antipsoriatic, antinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablility; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LKTOSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKIONSTFVRVHEK---DKTHTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTAC1(a) protein sequence.
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                                                                                         endothelial growth factor; VEGF; VEGF
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84.9%; Score 2069.5; DE
Best Local Similarity 85.7%; Pred. No. 3e-129;
Matches 395; Conservative 16; Mismatches 4
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                                                                                         Human; Flt1; vascular
                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy
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N-PSDB; ABQ74609.
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                                                                                                                                           This sequence represents a fusion protein of the invention between the Flt1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHN
                                                                                              AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                   PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                                                                                                                                                                    Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; 1gG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.1%; Score 2049; DB 4; Length 462;
84.2%; Pred. No. 7.1e-128;
.ive 13; Mismatches 47; Indels 14
                                                                                                                                                                                      YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 455
                                                                                                                                                                             YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                              Flt1 receptor fusion protein Mut3:Flt1(2-3)-Fc.
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                                                                                                                                                                                                                                                                                                          entry)
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Matches 393; Conservative
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N-PSDB; AAA91072.
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Human, Flt1, vascular endothelial growth factor, VEGF, VEGF antagonist, psoriasis, wound healing, Flt1 receptor, antipsoriatic, antiinflammatory, vulnerary, antiasthmatic, antiirheumatic, antiarthritic, nephrotropic; ophthalmological, vascular permeability, oedema, inflammation, asthma; brain oedema, inflammatory disorder; rheumatoid arthritis, burn, kidney disease, eye disorder, age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                              356 GQPREPQVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415
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                                  PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT
                                                     PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT
                                                                                                121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                         458
                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK
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                                                                  antimination measure, and antiagement, an authoritation, and infilammentory, vulnerary, antiagement, an authoritation methoric and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents Mut3:FlI(2-3) -FC which is used in an example from the present invention
               enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415
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                                                                                                                                                                                                                                                                                                                                                                                             47; Indels 14; Gaps
present invention describes a method for treating psoriasis and
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84.2%; Pred. No. 7.1e-128;
ive 13; Mismatches 47;
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Best Local Similarity 84.2<sup>3</sup>
Matches 393; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 452;
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83.9%; Pred. No. 3.7e-127;
iive 10; Mismatches 41;
                                                                                                                   Davis S, Yancopoulos GD;
                                                                                                                                                                                                                                                                    Claim 49; Fig 14; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP52444 standard; protein; 452
                            23-MAY-2000; 2000WO-US014142.
                                                         99US-0138133P
                                                                                     (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                               WPI; 2001-071076/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
392; Conserv
                                                                                                                   Papadopoulos NJ,
                                                                                                                                                                N-PSDB; AAA91071
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 452 AA;
                                                         08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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AC ABP5
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346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405
16 EIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a fusion protein of the invention between the Fl1 receptor and the Fc region of 1gG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                         DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                       352 GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
plasma leakage; vascular permeability; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                     DGSFFLYSKLTVDKSRWQQGNVFSCSVMHBALHUHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                            DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flt1 receptor fusion protein Mut4:Flt1(1-3R-N)-Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.5e-125;
14; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 2015.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVSYWDTGVLLCALLSCLLLTGSSSG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY97593 standard; protein; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAY-2000; 2000WO-US014142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGE-) REGENERON PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-071076/08.
N-PSDB; AAA91073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 567 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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Matches 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhancing wound healing in amammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating posciasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represent invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                  Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; antipsoriatic; antinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK------ 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIHMTEGRELVIPCRVTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention describes a method for treating psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating psoriasis and enhancing wound healing in humans comprises administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutation 2 Flt1(2-3 delta B)-Fc protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.6%; Score 2038; DB 5;
83.9%; Pred. No. 3.7e-127;
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(first entry)
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                                                                                                                                                                                                  kidney disease; eye
diabetic retinopathy
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Best Local Similarity
Matches 392; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rudge JS,
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                                                249
                                                                                                                                                    SVFLEPPKEKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNS 418
                                                                                                                                                                                                                       Human, Flt1; vascular endothelial growth factor, VEGF; VEGF antagonist, psoriasis; wound healing, Flt1 receptor; antipsoriatic; antinflammatory, vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; endema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration;
                                                                                                                         KLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKNASVRRR--IDQSNSHANIFYSVLTI 298
                                                                                                                                                                           SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
                                                                                                                                                                                                             TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
                                                                                                                                                                                                                                               TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
                      61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
                                                                        GKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGI
                                                                                                        ELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI
                                                                                                                                          DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK-----DKTHTCPPCPAPELLGGP
                                                                                                                                                                                                                                                                                                                                                                                            Mutation 4 Flt1(2-3 R->N)-Fc protein sequence.
                                                                                                                                                                                                                                                                                  QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                           QGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetic retinopathy
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N-PSDB; ABQ74607.
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Synthetic.
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antinificammatory, vulnerary, antiaethmatic, mentablematic, antianthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering vends attagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with injury, oedema associated with injury, oedema associated with injurant orders as praint of a sporders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents Mut4:Flt1(2-3 R
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                                                                                                                                                                                       enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 WSLPEMVSKESERLSITKSACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVPTSKKKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDTGRPFVEMYSEIPEIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                             present invention describes a method for treating psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.7%; Score 2015.5; DB 5; Length 567; 69.6%; Pred. No. 1.5e-125; ive 14; Mismatches 46; Indels 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ->N)-Fc which is used in an example from the present invention
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                                                                                                         Example 14; Fig 16A-D; 179pp; English.
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Best Local Similarity
Matches 396; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 567 AA;
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enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic, nephrorropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis; wound healing; Fltl receptor; antipsoriatic; antiinflammatory; vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeablility; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidhey disease; eye disorder; age-related macular degeneration;
                                                                                                                                                                                                              479 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF)
                            359 SVFLFPPKPKDTLMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                           310 TYRVVSVLTVIHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                   419 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                                                                                                                                                      370 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
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                                                                                                                                                                                                                                                                               430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                      539 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP52442 standard; protein; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flt1(1-3)-Fc protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-2002; 2002WO-US002466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JAN-2001; 2001US-00773877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic retinopathy.
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    250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP52442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xia Y,
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a fusion protein of the invention between the Pt1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Fl11 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD
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                                                                                                                                                                                   Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
plasma leakage; vascular permeability; IgG Fc region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.7%; Score 2014.5; DB 4 69.6%; Pred. No. 1.8e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yancopoulos GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Mismatches
                                                                                                                                        Flt1 receptor fusion protein Flt1(1-3)-Fc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVSYWDTGVLLCALLSCLLLTGSSSG-----
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AAY97597 standard; protein; 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papadopoulos NJ, Davis S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGE-) REGENERON PHARM INC
                                                                                           (first entry)
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Matches 396; Conserv
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                                             AAY97597
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                                                                                                                                                                                            SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
                                                                                                                                                                                                                                                                                                                                                                  SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418
                                                                                                                                                           61 WSLPEMVSKESERLSITKSACGRNGKQPCSTLTLNTAQANHTGPYSCKYLAVPTSKKKET 120
                                                                                                                                                                                                                                                                   BLSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
                                                                                                                                                                                                                                                                                                                                                                                               TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL 369
                                                                                                                                                                                                                                                                                                                                                                                                            TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SDTGRPFVEMYSEIPELIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 78
or vascular permeability. The present sequence represents Flt1(1-3)-Fc which is used in an example from the present invention
                                                                           Gaps
                                                                         47; Indels 113;
                                                    Length 567;
                                                                                              · 1 MVSYWDTGVLLCALLSCLLLTGSSSG------
                                                    DB 5;
                                                   82.7%; Score 2014.5; DB 569.6%; Pred. No. 1.8e-125; tive 13; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGNVFSCSVMHEALHNHYTQKSLSLSPGK 567
                                                 Query Match
Best Local Similarity 69.6*
Matches 396; Conservative
                               Sequence 567 AA;
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Search completed: September 23, 2005, 17:14:53 Job time : 125 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein September 23, 2005, 16:52:28 ; Search time 39 Seconds (without alignments) 1129.930 Million cell updates/sec Run on:

US-10-811-170-2 2437

Title: Perfect score:

1 MVSYWDTGVLLCALLSCLLL......MHEALHNHYTQKSLSLSPGK 458 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
1: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig gamma-1 chain C
Ig baavy chain V r
Ig gamma-1 chain C
Ig gamma-2 chain C
Ig gamma-3 chain C
Ig gamma 2b chain C
Ig gamma 2b chain C
Ig gamma 2c chain C
Ig gamma 2c chain C
Ig gamma 1 chain C
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-1 chain C
Ig gamma-3 chain C
Ig gamma-1 chain C
Ig gamma-2c chain
Ig gamma-2a chain
Ig gamma-2c chain Description SUMMARIES GHHU S69339 S31866 PT0207 G2HU A2351 G4HU A60764 G3HUWI I47159 GHRB I47159 GGRP I47162 I47161 I47161 S22080 G3MSC G3MSC PC4436 C30554 PS0018 S37483 G2MSA G1MS S00847 PS0017 Query Match Length DB 4446.9 4446.9 466.9 1240.5 1240.5 1233 1180 1148.5 1144 929.5 929.5 925.5 917.5 913.5 899.5 866.5 863.5 855.5 854.5 852 843.5 837.5 833.5 832.5 832.5 Score Result ٠ ک

Ig gamma-1 chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2b chain	Ig gamma-2a chain	Ig gamma-2b chain	soluble vascular e	protein-tyrosine k	Ig gamma-2b chain	Ig gamma-2 chain C	protein-tyrosine k	Ig gamma heavy cha	Fit-1 tyrosine kin	receptor tyrosine	embryonic receptor	To heavy chain V-T
SIMSM	S40295	G2MSAB	G2MS11	PS0019	G2MSBM	A49636	S09982	801321	806611	JC1402	146732	160598	178875	S49010	A36040
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393 1 (446 2	335 1	474 1	322 2	405 1	687 2	1338 2	475 2	327 2	1356 2	180 2	1336 2	1333 2	1330 2	218
		33.9 335 1					•					•	•		
34.0	33.9		33.2	33.1	33.0	32.9	32.9	32.5	31.7	29.7	29.0	28.7	27.9		23 0

ALIGNMENTS

KESULI I
ЭННО
Ig gamma-1 chain C region - human
S;Species: Homo sapiens (man)
2;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-20
3, Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A021
X; Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
4, Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A; Reference number: A93433; MUID:82274238; PMID:6287432
A; Accession: A93433
A; Molecule type: DNA
A;Residues: 1-330 <ell></ell>
A;Cross-references: UNIPROT:P01857; EMBL:Z17370
\note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the G
Note: Lys-330 is removed after translation .
X;Harris, L.J.
submitted to the EMBL Data Library, October 1992

nge 09-Jul-2004 A91723; A02146

ys, and the Glm(1) markers,

A; Reference number: S33904

A;Accession: S36861 A;Molecule type: DNA A;Residues: 2-330 <HAR>

A/Cross-references: EMBL:217370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a same structure of human immunoglobulin gamma genes: implications for evolution of a same scession; S33887

A/Rocession; S33887

A/Rocession; S33887

A/Rocession; S3887

A/Rocession; MulD:83001943; PMID:681139

A/Rocession; MulD:83001943; PMID:5489771

A/Rocession; S3887

A/Rocession; S38

A;Molecule type: protein
A;Residues: 1-56, R. /98-135 <CUN>
A;Residues: 1-56, R. /98-135 <CUN>
A;Note: this sequence has the Glm(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Bàchofmeinstry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842

A,Accession: A90564
A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Rosidues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, A;Rote: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
B,Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A,Title: Die Primaerstruktur eines monoklonalen IgGl-Immunglobulins (Myelomprotein Nie),

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A,Accession: S31866
A,Molecule type: mRNA
A,Residues: 1-255 <FIL>
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A; Reference number: A91668; MUID:77070269; PMID:826475
A; Contents: myeloma protein Nie
A; Reference number: A91668; MUID:77070269; PMID:826475
A; Contents: myeloma protein Nie
A; Accession: B91668
A; Molecule type: protein
A; Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A; Mote: this sequence has the Gim(1) and Gim(1) markers
A; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 198-38
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgGl KOL
A; Rocession: A91723
A; Title: Die Primaerstruktur des Kristallisierbaren monoklonalen Immunglobulins IgGl KOL
A; Rocession: A91723
A; Molecule type: protein
A; Residues: 1-96, 'R', 98-197,'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Residues: 1-96, 'R', 98-197,'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Residues: 1-96, 'R', 98-197,'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
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A; Residues: 1-96, 'R', MUID: 1064027; PMID: 108102129
A; Title: Rule of antibody structure of monoclonal IgGl immunocition of monocition of monocition of monocitic
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A/Genes Teferences: GDB:120085; OMIM:147100
A/Map position: 14q32.33-14q32.33
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1; 114/1; 224/1
A/Introns: 99/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/1; 114/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 TIDGVTRSDQGLYTCAA----SSGLMT------KKNSTFV--RVHEK--DKTHTCP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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Ig heavy chain V region precursor - human C;Species: Homo sapiens (man)

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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S7864
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Reference number: S79339
A;Coss-references: EMBL:X81695
R;Khamlichi, A.A.
A;Reference number: S72664
A;Reference number: S72664
A;Reference number: S72664
A;Reference number: S72664
A;Residues: 1-140, C',142-374 < KH2>
A;Roclaus: prellminary
A;Molecule type: mRNA
A;Residues: 1-140, C',142-374 < KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 QTITLITCTFSGFSLSKSGVGVGWIRQPPGQALEWLALIFWDDDKRYSPSLRTRLTITKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 KKFLSTLTIDGVTRSDQGLYTCAAS----SGLMTKK--NSTFVRVHEK----DKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 SKNOVVLTMTNVDPADTATYYCGYSVEGYGQGYRFHSWGQGTLVTVSSEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 PCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKÇKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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100.0%; Pred. No. 2.9e-71;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.9%; Score 1240.5; DB: Best Local Similarity 72.9%; Pred. No. 1.5e-71; Matches 248; Conservative 17; Mismatches 50
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Best Local Similarity 100.0
Matches 227; Conservative
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A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Mocleule type: protein
A;Residues: 1-19, 'Q', 21-57, 'Z', 59,'A', 61-193,'D', 195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
A;Note: Trp-156 is at or near the complement-binding site
B;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a }
A;Contents: myeloma protein Zie
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Nolecule type: protein
A;Residues: 1-24, 'E',2c-57, 'EV', 60-85;132-171, 'ZZZ', 175,'B', 177-193,'D', 195-196,'Q', 198-7;
A;Note: this sequence has since been revised
B;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin gs
A;Reference number: A93132; MUD:80114419; PMID:118920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic
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A;Map position: 14q32.33-14q32.33
A;Map position: Immunoglobulin heterotetramer; immunoglobulin
B;Generian: immunoglobulin homology <IMI>F;133-202,Domain: immunoglobulin homology <IMI>F;133-203,Domain: immunoglobulin homology <IMI>F;135-306,Domain: immunoglobulin homology <IMI>F;135-306,Domain: immunoglobulin homology <IMI>F;135-306,Domain: immunoglobulin homology (IMI)
F;135-306,Domain: immunoglobulin homology (IMI)
F;135-306,Dom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 VYTLPPSKDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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Biochem. J. 121, 217-225, 1971
A;Tile: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Tile: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; WIDD:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
B;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1569
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MID:69064124; PMID:5782707
C;Genetics: annotation; Sa, disulfide bonds
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80.0%; Pred. No. 9e-66;
Live 13; Mismatches 20; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: A93132
A,Molecule type: protein
A,Residues: 238-275 <HOF>
R,Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
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Best Local Similarity 80.0
Matches 224; Conservative
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C; Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C; Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
R; Fillison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con A; Reference number: A93906; MUID: 82197621; PMID: 6804948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-326 < ELL>
A; Residues: 1-326 < ELL>
A; Residues: UNID: GRILDA
A; Oroses references: UNID: UNID: GRILDA
B; Note: Lype-326 is probably removed posttranslationally
B; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
                                                                                                                                                                                                                                       89 GVEVHNAKTKPREEQYNSTYRVVSVLTVLAQDWLNGKEYKCKVSNKALPAPIEKTISKAK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKTHTCPPCPAPELLGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
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                                                                                                                                                                                        GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
                                                                                                                                                                                                                                                                                                                                                      GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gigeries: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiSpecies: Pan troglodytes (chimpanzee)
CiAccession: PT0207
RiEhrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A;Reference number: PT0207, MUID:91287716; PMID:2062315
A;Accession: PT0207
A;Rolecule type: mRNA
A;Residues: 1-234 <= MRNA
A;Residues: 1-234 <= MRNA
A;Residues: 1-234 <= MRNA
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin homology <= MRNA
                                                                                                                                                                                                                                                                                                                                                                                                     DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVUDVSHEDPEVKFNMYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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48.4%; Score 1180; DB 2; Length 234;
Best Local Similarity 98.6%; Pred. No. 6e-68;
Matches 217; Conservative 1; Mismatches 2; Indels
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A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:119340; OMIM:147130
A;Cross-references: GDB:111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp. hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into langing immunoglobulin C region; immunoglobulin homology circumary; immunoglobulin homology; circumary; immunoglobulin; interchain; immunoglobulin; homology; circumary; immunoglobulin; interchain; immunoglobulin; homology; circumary; immunoglobulin; interchain; interchain; immunoglobulin; interchain; interchain; immunoglobulin; interchain; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PAPELLGGPSVFLFFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 PAPEFLGGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 TLPPSQEEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 289
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C;Species: Homo sapiens (man)
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Fitle: A human immunoglobulin IGHG3 allele (Gmb0, bl, c3, c5, u) with an A;Reference number: A60764; MUID:90007613; PMID:2571587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 1144; DB 1; Length 327; 79.9%; Pred. No. 1.7e-65; tive 14; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 TIDGVTRSDQGLYTCAA----SSGLMTKKNSTFVRVHEKDKTHT--
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illarity 92.5%; Pred. No. 2.1e-65;
Conservative 8; Mismatches 9:
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A, Residues: 1-377 < HUC>
A, Cross references: UNIPROT: Q8N4Y9
C, Superfamily: immunocalation
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nes 222; Conservative
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Best Local Similarity
Matches 210; Conserv
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                                             Gene: GDB:IGHG4
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Matches
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                                                                                                                                                                                                                                                            RESULT 6
A2351

Iggard 3
A2351

Iggard 3
A2351

Iggard 3
A2351

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A2351
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: CA;Accession: A23511
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Residues: 1-377 - cHUC>
A;Residues: 1-377 - cHUC>
A;Residues: 1-377 - cHUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Generics:
A;Gene: GBB:IGHG3
A;Cross-references: GB:X130/3; 145/3; 160/3; 270/3
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Ksywords: immunoglobulin homology <IMM>
F;20-85/Domain: immunoglobulin
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G4HU

19 gamma-4 chain C region - human

C; Species: Homo sapiens (man)

C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C; Date: 02-Apr-1982 #sequence of a human immunoglobulin C-gamma4 gene.

B; Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A; Ricession: A90333 MUID: 83157104; PMID: 6299662

A; Accession: A9033

A; Molecule type: DNA

A; Residues: 1-377 cELL>
A; Cross-references: UNIPROT:P01861

A; Note: the sequence was determined from the germline gene
B; Diothem. J: 17, 33-47, 1970

A; Title: Human immunoglobulin sublclasses. Partial amino acid sequence of the constant r
A; Reference number: A90249; MUID: 70207560; PMID: 4192699

A; Molecule type: protein

A; Residues: 1-30; 81-326 <PIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 GVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTK 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           271 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330
227 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLY 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
47.0%; Score 1146; DB 2; Length 3
Best Local Similarity 92.5%; Pred. No. 1.5e-65;
Matches 210; Conservative 8; Mismatches 9; Indels
                                                                                                                            SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                              419
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Cyaccession: 147160
Rykacskovics, 1.; Sun, J.; Butler, J.E.
A,Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A; Reference number: 147160
A; Reference number: 147169; MUID:95015845; PMID:7930579
A; Rocession: 147160
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 VIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQGGGIFQCA 307
64 DTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVICVVUDVSHEDPEVQFKWYVD 123
                                                                                                                                                        143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTOSGSEMKKFLSTLTID 199
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147159, Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                      352 GOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                 184 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS
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                                                                                                                 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                       412 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 457
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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38.1%; Score 929.5;
Best Local Similarity 56.1%; Pred. No. 7.2e
Matches 180; Conservative 41; Mismatches
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A.Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-A; Corssion: A90442; MUID:81021548; PMID:6774747
A; Reference number: A90442; MUID:81021548; PMID:6774747
A; Molecule type: protein A; Ascession: A90442
A; Molecule type: protein A; Ascession: A90442
A; Mote: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Mote: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Mote: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Mote: the molecule is a fixed fixed the Vinge' region and all of the CHI region. Residue 12 cc A; Mote: the sequence of residues 42.76 was taken from the reference that follows R; Michaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the Vinge' region of human IgG3. Probable quadruplication A; Reference number: A92219; MUID:77118561; PMID:401363
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Note: a carboxyl-terminal Ly, 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter R,Nolfenstein-Todel, C.; Frandione, B.; Prelli, F.; Franklin, B.C.
Biochem. Biophys. Res. Commun. 71, 907-914, 1976
A,Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the A,Reference number: A90198; MUID:77021516; PMID:82345
A,Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues A,Roceasion: A90198
A,Nolecule type: protein
A,Residues: 59-125, EB',128-226,228-289 <WOL>
A,Note: this protein lacks most of the V region, all of the CH1 region, and part of the R,Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, B.C.; Hood, L.; Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A,Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion A,Reference number: A93915; MUID:82247835; PMID:6808505
A,Contents: heavy chain disease protein Omm
A,Accession: A93915
A,Note: a carboxyl-terminal Lys is removed posttranslationally
A,Note: a carboxyl-terminal Lys is removed posttranslationally
A,Note: a carboxyl-terminal Lys is removed posttranslationally
A,Note: a carboxyl-terminal Lys is shown.
C,Gemettics:
A,Contents: Hold Sease protein Wis is shown.
C,Gemettics:
A,Contents: AD3164418035.
A,Contents: AD3164418035.
A,Contents: AD3164418035.
A,Note: a carboxyl-terminal Lys is removed posttranslationally
A,Residues: C,Comment: The heavy chain disease protein Wis is shown.
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                                                                                  271 GOPREPQVYTLPPSREEMTKNQVSLICLVKGFYPSDIAVEWESSGQPENNYNTTPPVLDS 330
                                               411
                                               GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F;203-270/Domain: immunoglobulin homology <IMM>
F;103-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                   46.0%; Score 1121; DB 1; Length 289; 90.3%; Pred. No. 4.3e-64;
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Matches 204; Conservative
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Same of Same

232 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291

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194 STLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCP-APELLG-GPSV
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C;Superfamily
F;82-151/Doma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 <MAR>
A; Cross-references: G8 M16426; NID:g165111; PIDN: AAA31289.1; PID:g165112
A; Note: this sequence has the dil allotypic marker, 104-Met, and the e15 allotypic marke
R; Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e14 marker, 185-Thr
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A,Accession: 147159
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-328 <KAC>
A,Cross-treferences: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 GEKLVLNCTARTELNVGIDFNWE---YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 GVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPCPAPELLGGPSVFLFPPKPK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DILMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSTYRVVSVLTV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 VIGEYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKASWQGGGIFQCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 QHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEELSRSKVSITCL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----QPSGLYSLSSMVTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                                                            A;Gene: IgG2a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Indels
                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPNVALGCLASSYFPEPVTVTWNSGALSSGVHTFPSVL-
                                                                                                                                                                                                                                                                                                                                                                                                 Score 929.5; DB 2 Pred. No. 7.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 VMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 56.1%;
Matches 180; Conservative 4:
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A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin (A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin (A;Reference number: A90245; MUD:70110015; PMID:5461106

A;Recession: A90245; MUD:70110015; PMID:5461106

A;Rolecule type: protein

A;Residues: 132-143, 'E', 145-161 <FRU>
R;Hill, R.L., Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

R;Hill, R.L., Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.

A;Reference number: A94416

A;Recession: A94416

A;Rocession: A94416

A;Rocession:
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Reference number: I47158; MUID: 95015845; PMID: 7930579
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-277 < KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma 4 chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: I47162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 VYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 TLTIDGV----TRSDQGLYTCAA----SSGLMTKKNSTFVRVHEK-DKT---HTC--P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 277;
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F;173/Binding site: carbohydrate
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A;Accession: 949553
A;Molecule type: protein
A;Residues: 1.3 < TIL>
A;Coss = references: UNIPROT: P01862
B;Eirshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am)
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 4-68 cHIR-
B;Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
Biochemistry 10, 9-17, 1971
Biochemistry 10, 9-17, 1973
A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir A;Reference number: A90359; MUID:71058486; PMID:5538616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Accession: A90385
A.Molecule type: protein
A.Residues: 227-311 c-TR2>
A.Molecule type: protein
A.Residues: 227-311 c-TR2>
R.Oliveira, B.; Lamm, M.E.
B.ochemistry 10, 26-31, 1971
A.Title: Interchalin disulfide bridges of guinea pig gamma-2- immunoglobulin.
A.Reference number: A90354; MUID:71058474; PMID:4922544
A.Contents: annotation; disulfide bonds
A.Note: Cys-16 is involved in a heavy-light chain bond
A.Note: Cys-107, and Cys-110 form inter-heavy chain bonds
C.Complex: An immunoglobulin heterofertamer subunit consists of two identical light (Rapy C.Complex: An immunoglobulin heterofertamer subunit consists of two identical light (Rapy C.Superfamily: immunoglobulin C region; immunoglobulin homology cimenoglobulin constitution immunoglobulin homology cimenoglobulin constitution constitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  guinea pig IgG2 antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 GSMMTLGCLVKGYFPEPVTVKWNSGALTSGVHTFPAVL-----QSG--LYSLTSMVTVP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 GVTRSDQGLYTC-AASSGLMTKKNSTF--VRVHEKDKTHTCPPCPAPELLGGPSVFLFPP
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A,Molecule type: protein
A,Residues: 69-13;312-329 <TUR>
B,Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A,Title: Primary structure of the C-H2 homology region from A,Reference number: A90384; MUID:75036072; PMID:4429665
C;Accession: A94553; A90352; A90359; A90384; A90385; A02151 R;Trischmann, T.M. submitted to the Atlas, April 1975 A;Reference number: A94553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: A90384
A, Molecule type: protein
A, Residues: 134-226 CTRA>
R, Trisichmann, T.M. Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A, Title: Primary structure of the C-H3 homology region f
A, Reference number: A90385; MUID:75036073; PMID:4609467
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Best Local Similarity 55.7%; Pred. No. 5.4e-
Matches 180; Conservative 38; Mismatches
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147158

(gramma 1 chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21.Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: 147158

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of A;Reference number: 147158

A;Accession: 147158
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                                                                                                                                                                                                                                                                                      SKYTLICLVYGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKLAVDKASWQ 248
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                                                                                                                           NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GEKLVLNCTARTELNVGIDFNWE----YPSSKHQHKKLVNRDLKTQSGSEMKKFLSTLTID 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DILMISRTPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 QHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTLTCL 247
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                                                                                                                                                                                                                                          RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 371
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               16 SMVTVPASSLSSKS-YTCNVNHPATTTK-----VDKRVGTKTKPPCPICPACEGPGPSA 68
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C;Species: Cavia porcellus (guinea pig)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GPNVALGCLASSYFPEPVTVTWNSGALTSGVHTFPSVL-----QPSGLYSLSSMVTVP
                                                                                           FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <1MM>
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A;Molecule type: mRNA
A;Residues: 1-128 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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759.762 Million cell updates/sec
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ALIGNMENTS

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Sequence 26, Application US/09773877B
Patent No. 683349
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION UMBER: US/09/773,877B
CURRENT PILING DATE: 2011-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 458 ö Length 458; Indels 100.0%; Score 2437; DB 4; 100.0%; Pred. No. 1.3e-196; ive 0; Mismatches 0; OTHER INFORMATION: VEGFRIR2-FcdeltaCl(a) Receptor TYPE: PRT ORGANISM: Artificial Sequence Best Local Similarity 100. Matches 458; Conservative

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61 FIISNATYKEIGLLICEATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLN 120
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Patent No. 6833349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REPRENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 24
SEQ ID NO 24
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                                                                                                                                                                                                                                     Score 2261; DB 4;
Pred. No. 7.5e-182;
0; Mismatches 0;
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84.9%; Score 2069.5; DB

Best Local Similarity 85.7%; Pred. No. 1e-165;

Matches 395; Conservative 16; Mismatches 41
                    NUMBER OF SEQ ID NOS: 27
SOFWARE: Patentin version 3.0
SEQ ID NO 27
EBNCTH: 431
                                                                                                                                                                                                                                     92.8%;
Local Similarity 99.1%;
les 428; Conservative (
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ORGANISM: Artificial Sequence
                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                      CTHER INFORMATION: Peptide US-09-773-8778-27
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      CURRENT FILING DATE:
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Matches
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361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: Xia, Yu-Ping et al.

TITLE OF INVENTION: METHODS FOR TREATING INFLANMATORY SKIN DISEASES
TITLE OF INVENTION: METHODS FOR TREATING INFLANMATORY SKIN DISEASES
FILE REFERENCE: RE7
CURRENT APPLICATION NUMBER: US/09/773,877B

CURRENT FILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.0

SEQ ID NO 22

LENGTH: 458
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Patent No. 6833349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 7109 V099773,877B
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                                                                         LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
                                          LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                      Sequence 22, Application US/09773877B
Patent No. 6833349
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Best Local Similarity 98.7%;
Matches 455; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                  RESULT 2
US-09-773-877B-22
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US-09-773-877B-27
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; OTHER INFORMATION: Flt1(2-3 deltaB)-Fc
US-09-773-877B-16
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                                                                                                           PPCPAPELLGGPSVFLFPPKDXDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 294
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                                        PNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120
                                                       HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180
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 1 MVSYWDTGVLLCALLSCLLLTGSSSG---GRPFVEMYSEIPEIIHMTEGRELVIPCRVTS
                                                                                                                                              181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 18
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84.1%; Score 2049; DB 4;
Best Local Similarity 84.2%; Pred. No. 5.6e-164;
Matches 393; Conservative 13; Mismatches 47;
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US-09-773-877B-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/09773877B; Patent No. 6833349; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-773-877B-18
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231 166 BIDQSNSHANIFYSVLTIDKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSC 225 291 285 411 356 GOPREPOVYILPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 415 PNITVTLKKRPPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLT 120 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351 GOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS 411 346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 405 351 1 MVSYWDTGVLLCALLSCLLTGSSSG---GRPFVEMYSEIPEIHMTEGRELVIPCRVTS 57 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 296 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAK GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 352 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK-----1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 24; Gaps Sequence 16, Application US/09773877B

Patent No. 683349

GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b

CURRENT APPLICATION NUMBER: US/09/773,877B

CURRENT FILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.0 458 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 452 | DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462 Length 452; DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458 Indels DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK Query Match 83.6%; Score 2038; DB 4; Best Local Similarity 83.9%; Pred. No. 4.6e-163; Matches 392; Conservative 10; Mismatches 41;

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                      Sequence 20, Application US/09773877B
Patent No. 6833349
GENERAL INFORMATION:
TITLE OF INVENT: Xia, Yu-Ping et al.
TITLE OF INVENT: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 201-01-31
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 20
LENGTH: 567
                                                                                                                                                                                                                                                                                                        46; Indels 113;
                                                                                                                                                                                                                                                                              Length 567;
                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                            82.7%; Score 2015.5; DB 4; 69.6%; Pred. No. 4.9e-161; Live 14; Mismatches 46;
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                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 396; Conservative
RESULT 7
US-09-773-877B-20
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US-09-773-877B-12
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Sequence 12, Application US/09773877B
Patent No. 6833349
GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b

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121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPD 180
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Sequence 14, Application US/09773877B

Sequence 14, Application US/09773877B

Sequence 14, Application US/09773877B

Tarte No. 683327B

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

FILE REFERENCE: REG 710b

CURRENT APPLICATION NUMBER: US/09/773,877B

CURRENT APPLICATION NUMBER: US/09/773,877B

SOFTWARE: PATCHIN OF 27

SOFTWARE: PATCHIN Version 3.0

SEQ ID NO 14

LENGTH: 557

TYPE: PRT

TYPE: PRT

CORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/09/773,877B
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MVSYWDTGVLLCALLSCLLLTGSSSG
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US-09-773-877B-12
                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
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FRAGMENT TYPE:
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                                                               DB 4; Length 557;
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Protein
                                                             Query Match 82.2%; Score 2003.5; DB 4 Best Local Similarity 69.4%; Pred. No. 4.9e-160; Matches 395; Conservative 10; Mismatches 41;
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Patent No. 6130202
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
TITLE OF INVENTION: Multimeric Forms of Hum;
TITLE OF INVENTION: Rainovirus Receptor From Correspondence Address:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 400 Morgan Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 1.44 Mb storage
COMPUTER: Dell Optiplex GXI
OPERATING SYSTEM: Windows 95
SUSTWARR: WORDPEFECT 8.0 for Windows
CSOFTWARR: APPLICATION DATA:
APPLICATION NUMBER: US/08/227,496C
             ; OTHER INFORMATION: Flt1(1-3 deltaB)-Fc (Mut1)
US-09-773-877B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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STATE: Connectic
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US-08-227-496C-15
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261 LTCAVILGNQSQETL--QTVTIXSPPAPNVILTKPEVSEGTEVTVKCE-AHPRAKVTLNG 317
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OTHER INFORMATION: amino acid residues 1-453 =
OTHER INFORMATION: tICAM(453); amino acid residues 454-680 = amino
OTHER INFORMATION: acid residues 216-442 of human IgG1 heavy chain
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CLASSIPICATION: 514
CLASSIPICATION: 514
PRIOR APPLICATION DAPA:
APPLICATION NUMBER: 07/903,069
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/704,984
FILING DATE: 05/34/91
APPLICATION NUMBER: 07/556,238
FILING DATE: 07/20/90
ATTORNEY/AGENT INFORMATION:
NAME: Barbara A. Shimei:
REGISTRATION NUMBER: 29,862
REFERRICE/DOCKET NUMBER: 39,862
REPERRICE/DOCKET NUMBER: 29,862
RELEPHONE: (203) 812-5492
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 680 amino acid residues
TYPE: amino acids
TYPE: amino acids
TYPE: mino acids
TYPE: mino acids
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287; Conservative
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US-09-313-942-28
                                               Similarity
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US-09-499-846-2
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                                                                                                                                                                                                                                                                                                                                                                                                            60 PSSGTPNPTLRWLK------NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                              ----EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 IVENEYGSIN-HTYQ-----LDVVERSPHRPILQAG----LPANKTVALGSNV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 DFNWEYPSSKHQHKKLVN-------RDLKTQSGSEMKKFLSTLTIDGVTR 203
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                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                               Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDQGLYTCAASSGLMTKKNSTFVRVHEK---------
                                                                                                                                                                                                                                             52.5%; Score 1280; DB 4; Length 4
54.3%; Pred. No. 2.9e-99;
ive 32; Mismatches 109; Indels
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          APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASELSEQ for Windows Version 3.0
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; Patent No. 6656728
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: 035784/195012 (5784-
CURRENT APPLICATION WUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
: LENGTH: 622
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.3%
Matches 284; Conservative
                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                             LENGTH: 497
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US-09-499-846-2
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                                                                                                                                                                              147
                                                                                                                                                                                                                                                                                                                                                            R-KGFIISNATYKEI-----GLLTC----EATVNGHLYKTNYLTHRQTNTIIDVV 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC 378
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                                                                                                                                                                                                                                         98
                                                                                                                                                        483 VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSKDELTKNQVSLTC
                                                                                                                                                                                                                                         ----VIPCRVT-----SPNITVTLKKFPLDTLIPDGKRIIWDS
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                                                                                                                   6 DIGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIP-----EIIHMTEGREL-----
                                                           Gaps
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Patent No. 6472179
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING TITLE OF INVENTION: AND USING TITLE OF INVENTION: AND USING CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1999-05-19
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-19
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Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 LSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVN----
                                                                                                                                                                                                                                                                                                                                                                                                        200 RIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSIN-HTYQ-----
                                                           Indels
DB 4;
                                                           34; Mismatches 100;
52.5%; Score 1279.5; DB 51.2%; Pred. No. 4.5e-99
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHEALHNHYTQKSLSLSPGK 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHEALHNHYTQKSLSLSPGK 458
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Best Local Similarity 63.55
Matches 257; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPNWEYPSSKHQHKKLVN-------RDLKTQSGSEMKKFLSTLTIDGVTR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 EQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 IVENEYGSIN-HTYQ-----LDVVERSPHRPILQAG----LPANKTVALGSNV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 PSSCTPNPTLRWLK-----NGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WKCLLFWAVLVTATLCTARPSPTLPEQP-VAPYWTSPE---KMEKKLHAVPAAKTVKFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DKTHTCPPCPAPE
300 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                367 TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 ----SPNITVTLKKFPLDTLIPDGKRIIWDSR-KGFIISNATYKEI------GLLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 WDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPELIHMTEGRELVIPCRVT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                       KLTVDKSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                          FUSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.1%; Score 1269.5; DB 4; Best Local Similarity 54.9%; Pred. No. 2.2e-98; Matches 282; Conservative 32; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 SDQGLYTCAASSGLMTKKNSTFVRVHEK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSRWQQGNVFSCSVWHEALHNHYTQKSLSLSPGK 488
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                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN 18 THE REPERENCE: 035784/195012 (5784-CURRENT APPLICATION NUMBER: US/09/499,846 CURRENT FILING DATE: 2000-02-07 SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/09499846; Patent No. 6656728; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Homo sapiens
US-09-499-846-12
                                                                                                                                                                                                                                                      RESULT 15
US-09-499-846-12
                                                                                                                                                       420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- DKTHTCPP 239
                                                                                                                     PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLEGSGSPGLQEPKSCDKTHTCPP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 366
                                                511 DCKPLLLDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENK
                                                                                                                                                                                                                                                                           PREPQVYILPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                      THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EATVNGHLYKTNYLTHRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNW
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                                                                                               TIIDVVLSPSH-GIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRDLKTQ
                                                                                                                                                                       SGSEMKKFLSTLTIDGVTRSDQGLY----TCAASS--GLMTKKNSTFVRV-----HEKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 SPNITVTLKKFPLDTLIPDGKRIIWDSR-KGFIISNATYKBI------GLLTC----
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                    DGKRIIWDS-----RKGFIISNATYKEIGLLTCEA--TVNGHLYK-
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Patent No. 6656728

GENERAL INFORMATION:
APPLICANT: KAVADAUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE REPRENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499, 846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-499-846-4
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US-09-499-846-4
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Best Local S
Matches 271
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                                                                                                                             September 23, 2005, 17:12:57; Search time 123 Seconds (without alignments) 1515.541 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         1 MVSYWDTGVLLCALLSCLLL.......MHEALHNHYTQKSLSLSPGK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence Sequence Sequence Sequence Sequence
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1: /cgn2_6/ptodata/2/pubpaa/NSO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/NSO6_NBW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_NBW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO1_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-830-902-2
US-10-890-802-2
US-10-909-011-4
US-10-988-243-16
US-10-988-881-4
US-11-016-097-16
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US-10-609-775-10
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-09-773-8774-26

Sequence 26, Application US/09773877A

Publication No. US2030017977A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

FILE REFERENCE: REG 710b

CURRENT APPLICATION NOSE: 27

NUMBER OF SEQ ID NOS: 27
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Pred. No. 3.5e-152;
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100.0%; Score 2437;
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 458; Conservative 0; Mismatches
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SEQ ID NO 26
LENGTH: 458
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                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10860958

Publication No. US20040265309A1

GENERAL INPORMATION:
APPLICANT: Kandel, Jessica
APPLICANT: Holash, Jocelyn
APPLICANT: Hanshiro, Darrell
APPLICANT: Tancopoulos, George
APPLICANT: Annopoulos, George
APPLICANT: Andee, John
TITLE OF INVENTION: Inhibitors
FILE REFERENCE: REG 714A
CURRENT APPLICATION UNMBER: US/10/860,958
CURRENT FILING DATE: 2004-06-06
PRIOR APPLICATION NUMBER: 60/476,425
PRIOR APPLICATION NUMBER: 60/476,425
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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JAPPLICANT: Thomas J. Daly

APPLICANT: James P. Fandl

APPLICANT: Thomas J. Papadopoulos

TITLE OF INVENTION: VGF TRAPS AND THERAPEUTIC USES THEREOF

FILE REFERENCE: REG 710D

CURRENT APPLICATION NUMBER: US/10/609,775

CURRENT FILING DATE: 2001-06-30

PRIOR APPLICATION NUMBER: PCT/USO0/14142

PRIOR PELLING DATE: 2000-05-23

PRIOR PELLING DATE: 1999-06-08

PRIOR FILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
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100.0%; Score 2437; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 10, Application US/10609775; Publication No. US20040014667A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-10-609-775-10
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                                                                                                                                                                                                                                                     Length 458;
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; Sequence 10, Incordant 10, 1020050043236A1
; Publication No. US20050043236A1
; GARERAL INFORMATION:
APPLICANT: Daly, thomas J.
APPLICANT: Pandl, James P.
APPLICANT: Pandl, James P.
ITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
FILE REFERENCE: RG 71002
CURRENT PRILING DATE: 2004-06-29
FRIOR PILING DATE: 2004-06-29
FRIOR PILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 29
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100.0%; Score 2437; DB 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; 1
                                                                                                                                                                                                                                              Query Match
100.0%; Score 2437; DB 17;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 458
  2004-07-23
                                                                                                                                                       TYPE: PRT
CRGANISM: homo sapiens
US-10-897-802-2
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CRGANISM: homo sapiens
US-10-880-021-10
CURRENT FILING DATE:
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Publication No. US20050032699A1
GENERAL INFORMATION:
APPLICANT: Jocelyn Holash
APPLICANT: Limin Hu
APPLICANT: Limin Hu
APPLICANT: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
FILE REFERENCE: REG 7158
CURRENT APPLICATION NUMBER: US/10/897,802
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                                                                                                                                                                           APPLICANT: Stanley Wiegand
APPLICANT: Stanley Wiegand
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
APPLICANT: Jingtai Cao
TITLE OF INVENTION: Method Treating Corneal Transplant
TITLE OF INVENTION: Method on
FILE REFERENCE: REG 713B
FULE APPLICATION NUMBER: US/10/830,902
CURRENT FILING DATE: 2004-04-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                            Sequence 2, Application US/10830902; Publication No. US20050004027A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homo sapiens
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LENGTH: 458
                                                                                           US-10-830-902-2
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US-10-897-802-2
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RESULT 8

US-10-988-243-16

US-10-988-243-16

Sequence 16, Application US/10988243

Publication No. US20050175610A1

GENERAL INFORMATION:

APPLICANT: Wiegand, Stanley

APPLICANT: Wiegand, Stanley

APPLICANT: Wiegand, Stanley

APPLICANT: Wancopoulos, Micholas J.

APPLICANT: Wancopoulos, George

TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinectic Prop.

TITLE OF INVENTION: and Methods of Making and Using Thereof

TITLE OF INVENTION NUMBER: 10/0988,243

CURRENT APPLICATION NUMBER: 10/099,852

PRIOR APPLICATION NUMBER: 10/009,852

PRIOR APPLICATION NUMBER: E07/US00/14142

PRIOR APPLICATION NUMBER: 60/138,133

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 1999-06-08

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 16

SEQ ID NO 16

LENGTH: 458
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     LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC
                                      PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
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100.0%; Score 2437; DB 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Sequence 4, Application US/10909011

Sequence 4, Application VS. US20050112061A1

GENERAL INFORMATION:

APPLICANT: JOCALYN HOLASH

APPLICANT: Bandy Burd

TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy

FILE REFRENCE: REG 716A

CURRENT FILING DATE: 2004-07-30

PRIOR PILING DATE: 2003-08-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PASCEC for Windows Version 4.0

FEAST OF ACCURACY AND APPLICANT OF A SECSION ACCURACY AND A
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Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                   APPLICANT: NICHOLAS J. Papadopoulos et al.
TITLE OF INVENTION: PHARMACKINETIC PROLYBETIDES WITH IMPROVED
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: PHARMACKINETIC PROPERTIES AND METHODS OF MAKING
TITLE OF INVENTION: AND USING THEREOF
FILE REFERENCE: REG 710-A-US
CURRENT PEPLICATION NUMBER: US/11/016,097
CURRENT FILING DATE: 2004-12-17
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-13-06
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 1999-06-08
PRIOR FILING DATE: 1999-06-08
SOFTWARE: FastSEQ for Windows Version 3.0
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  421 LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
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                                                                                                        Sequence 16, Application US/11016097; Publication No. US20050163798A1; GENERAL INFORMATION:
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US-11-039-144-2
US-11-039-144-2
; Publication No. US20050197291A1
; GENERAL INFORMATION:
APPLICANT: Stanley Wiegand
; APPLICANT: Jingtai Cao
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Matches 458; Conservative
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                                                               RESULT 10
US-11-016-097-16
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APPLICANT: Jocelyn Holash
APPLICANT: Jocelyn Holash
APPLICANT: George Yancopoulos
APPLICANT: Adam P. Dicker
APPLICANT: Adam P. Dicker
APPLICANT: Randy Burd
TITLE OF INVERTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
FILE REPERENCE: 7168
CURRENT APPLICATION NUMBER: 10/909,011
FRIDE REPLICATION NUMBER: 10/909,011
PRIOR FILING DATE: 2004-07-30
PRIOR FILING DATE: 2004-07-30
PRIOR PILING DATE: 2003-08-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAEKSEQ for Windows Version 4.0
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                        KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360
                                                                                   TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
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                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/1099881; Publication No. US20050196340A1; GENERAL INFORMATION:
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ORGANISM: homo sapiens
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Sequence 8, Application US/10609775 Publication No. US20040014667A1
                                           98.4%;
98.7%;
                                          Query Match
Best Local Similarity 98.7
Matches 455; Conservative
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Best Local Similarity 98.7
Matches 455; Conservative
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; ORGANISM: homo sapiens
US-10-609-775-8
         US-09-773-877A-22
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US-10-609-775-8
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENGTH: 458
APPLICANT: Claus Cursiefien
TITLE OF INVENTION: Method of Treating Corneal Transplant
TITLE OF INVENTION: Rejection in High Risk Keratoplasty Patients
FILE SPERENCE: 713C
CURRENT PILING DATE: 2005-01-19
PRIOR APPLICATION NUMBER: 10/830,902
PRIOR PILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2003-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FREEEEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: F1t1D2.F1k1D3.FcdeltaC1(a) Receptor
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US-09-773-877A-22
Sequence 22, Application US/09773877A
Publication No. US20030017977A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 458; Conservative
                                                                                                                                                                                                                                   LENGTH: 458
TYPE: PRT
ORGANISM: homo sapiens
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                                                                                                                         1 MVSYWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS
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APPLICANT: Thomas J. Daly
APPLICANT: Thomas J. Daly
APPLICANT: Thomas J. Daly
APPLICANT: James P. Fand
APPLICANT: James P. Rand
TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
FILE REFERENCE: REG 710D
CURRENT APPLICATION NUMBER: 10/009,852
PRIOR PILING DATE: 2003-06-30
PRIOR APPLICATION NUMBER: 10/009,852
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 1000-05-23
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ 1D NOS: 25
NUMBER OF SEQ 1D NOS: 25
   Length 458;
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98.7%; Pred. No. 1.1e-149;
iive 0; Mismatches 0;
Score 2399; DB 10;
Pred. No. 1.1e-149;
                                                            0; Mismatches
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Db 238 PPCPAPELLGGPSVFLPPPKPXDTLMISRTPBVTCVVVDV8HEDPEVKFNWYVDGVEVHN 297 Qy 298 AKTKPREEGYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357 Db 298 AKTKPREEGYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357 Qy 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417 Qy 418 YSKLTVDKSRWQCGNVFSCSVMHEALHNHYTQKSLSLSPGK 458	CURRENT FILING DATE: 2004-07-3 PRIOR APPLICATION NUMBER: 60/4 PRIOR FILING DATE: 2003-08-06 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows V SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: homo sapiens COGANISM: homo sapiens S-10-909-011-2	Local Similarity 98.7%; Pred. No. 1.1e-149 98 455; Conservative 0; Mismatches 0 1 MVSYMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYS 1 MVSYMDTGVLLCALLSCLLLTGSSSGSDCRPFVEMYS 61 PNITVTLKRPLDTLPDGRRIIMDSRKGFIISNATYK	Qy 121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELNVGIDFNWEYPSSKHQHKKLVNRD 180 	Qy 181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC 237 	QY 238 PPCPAPELLGGPSVFLFPPKPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297	Qy 298 AKTKPREEQYNSTYRVUSULTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357 	Qy 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417	Qy 418 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 458
	RESULT 14 US-10-880-021-8 ; Sequence 8, Application US/10880021 ; Publication No. US20050043236A1 ; GENERAL INFORMATION: ; APPLICANT: Daly, thomas J. ; APPLICANT: Pandl, James P. ; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof ; FILE REFERENCE: RGE 710D2 ; CURRENT APPLICATION NUMBER: US/10/880,021	CURRANT FILING DATE: 2004-06-29 PRIOR APPLICATION NUMBER: 10/609,775 PRIOR FILING DATE: 2003-06-30 NUMBER OF SEQ ID NOS: 29 SEQ ID NO 8 LENGTH: 458 TYPE: PRI TYPE: PRI ORGANISM: homo sapiens US-10-880-021-8	Query Match 98.4%; Score 2399; DB 17; Length 458; Best Local Similarity 98.7%; Pred. No. 1.1e-149; Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;	Qy 1 MVSYMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTEGRELVIPCRVTS 60	Qy 61 PNITVTLKKFPLDTLIPDGKRIUWDSRKGFIISNATYKEIGLLTCBATVNGHLYKINYLT 120 	Qy 121 HRQTNTIIDVVLSPSHGIELSVGEKLVLNCTARTELAVGIDFNWEYPSSKHQHKKLVNRD 180 	OY 181 LKTOSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC 237	Qy 238 PPCPAPELLGGPSVFLFPFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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